

Table III

Gene Name	Coriell DNA Panel(s)	Amplicon No.	Total SNPs	Missense	Silent	UTR	Intronic
Aminopeptidase P (XPNPEP2)	24 + 47 (55AA) + 12pt	24	30	0	2	7	21
Bradykinin B1 receptor (BDKRB1)	24+ 95 (8AA, 103 CAU) + 12pt	7	14	2	5	3	4
Bradykinin B2 receptor (BDKRB2)	24 (8AA) + 12pt	12	36	3	2	14	17
NK1 tachykinin receptor (TACR1)	24 (8AA) + 12pt	7	9	0	3	3	3
C1 esterase inhibitor (CINH)	24 (8AA) + 12pt	10	6	2	2	0	2
Kallikrein 1 (KLK1)	7 (7AA) + 12pt	5	6	1	1	2	2
Protease Inhibitor 4 (PI4)	7 (7AA) + 12pt	8	12	1	3	1	7
Angiotensin Converting Enzyme 2 (ACE2)	7 (7AA) + 12pt	20	9	0	0	0	9
Totals:			122	9	18	30	65

Table IV (1 of 2)

[illegible]

Table IV (2 of 2)

GENE DESCRIPTION	HOMIC ID	SNP ID	CONTRD	MAJL	CONTRD POS	FLANK SEQ (REF/ALT)	FLANK SEQ REF	SEQ ID NO.	FLANK SEQ ALT	REF SEQ ID NO.	REF SEQ POS	REF	ALT	REF	ALT	EXON	MUTATION TYPE	REVCOMP	REF	CONTRD ALT	CONTRD SEQ ID NO.	CONTRD SEQ POS
BovHNF2	AE100427	4	1828	ABSTTGGA	C/T	GATGTGGCA	592	AL551022	594	AL551022	62978	G	A	Exon2	Non-CDS	1			GA	594	NM_000623.1	1877
BovHNF2	AE100428	4	2102	TGAGGATC	C/T	TTCGACAGA	593	AL551022	595	AL551022	62979	G	A	Exon2	Non-CDS	1			GA	595	NM_000623.1	2117
BovHNF2	AE100429	4	2238	AGTTCG	A/G	CTGCTGGT	594	AL551022	596	AL551022	62980	G	A	Exon2	Non-CDS	1			GA	596	NM_000623.1	2254
ACE2	AE100430	10	37	ATGATGAT	A/G	TAAATATAT	595	AD008983	597	AD008983	88172	C	A	Intron14	Non-CDS	1			GA	597	NM_000623.1	
ACE2	AE100431	10	290	ATTGACAA	C/G	TACTCAGCG	596	AD008983	598	AD008983	88173	C	T	Intron14	Non-CDS	1			GA	598	NM_000623.1	
ACE2	AE100432	11	282	ATTATGAC	C/T	TACTCAGGT	597	AD008983	599	AD008983	88424	C	G	Intron19	Non-CDS	1			GA	599	NM_000623.1	
ACE2	AE100433	11	440	GATCTCTA	T/G	ATAAAGATA	598	AD008983	600	AD008983	88425	C	G	Intron19	Non-CDS	1			GA	600	NM_000623.1	
ACE2	AE100434	15	109	AGATATGG	C/T	TGCGACAGA	599	AD008983	601	AD008983	88426	C	G	Intron19	Non-CDS	1			GA	601	NM_000623.1	
ACE2	AE100435	15	109	AGATATGG	C/T	TGCGACAGA	600	AD008983	602	AD008983	88427	C	G	Intron19	Non-CDS	1			GA	602	NM_000623.1	
ACE2	AE100436	15	441	GGTCTGCA	T/A	GTCTCTGTG	601	AD008983	603	AD008983	88428	C	G	Intron19	Non-CDS	1			GA	603	NM_000623.1	
ACE2	AE100437	15	441	GGTCTGCA	T/A	GTCTCTGTG	602	AD008983	604	AD008983	88429	C	G	Intron19	Non-CDS	1			GA	604	NM_000623.1	
ACE2	AE100438	2	129	GAAAGACT	A/G	TATGTGAT	603	AD008983	605	AD008983	88430	C	T	Exon2	Non-CDS	1			GA	605	NM_000623.1	
ACE2	AE100439	3	189	GATTTABA	A/G	CATTATG	604	AD008983	606	AD008983	88431	C	T	Exon2	Non-CDS	1			GA	606	NM_000623.1	
ACE2	AE100440	3	290	CGACAAAC	T/A	GTCTGCG	605	AD008983	607	AD008983	88432	C	T	Exon2	Non-CDS	1			GA	607	NM_000623.1	
ACE2	AE100441	4	583	CTTGAGTCT	A/G	GTGACAAATC	606	AD008983	608	AD008983	88433	C	T	Exon2	Non-CDS	1			GA	608	NM_000623.1	
ACE2	AE100442	4	1828	GAGGATGG	T/T	ATCTCAGAA	607	AD008983	609	AD008983	88434	C	T	Exon2	Non-CDS	1			GA	609	NM_000623.1	
ACE2	AE100443	4	607	GGTCTG	A/G	CTGCTGAA	608	AD008983	610	AD008983	88435	C	T	Exon2	Non-CDS	1			GA	610	NM_000623.1	
ACE2	AE100444	4	1815	CGAAATGG	T/G	GGTGATAG	609	AD008983	611	AD008983	88436	C	T	Exon2	Non-CDS	1			GA	611	NM_000623.1	
ACE2	AE100445	4	2020	TGTTTGTT	G/C	GTGTTTGT	610	AD008983	612	AD008983	88437	C	G	Exon2	Non-CDS	1			GA	612	NM_000623.1	
XPNPEP2	AE100043	6	389	GAGCGAGG	T/A	AGAGTCTG	611	AD008983	613	AD008983	88438	C	T	Exon2	Non-CDS	1			GA	613	NM_000623.1	
XPNPEP2	AE100045	13	659	CGTAAAGG	C/T	GTGAGAGT	612	AD008983	614	AD008983	88439	C	T	Exon2	Non-CDS	1			GA	614	NM_000623.1	
XPNPEP2	AE100028	13	181	ACACAGAT	T/G	CCACACAGG	609	AD008983	615	AD008983	79758	G	T	Intron13	Non-CDS	0			GA	615	NM_000623.1	
XPNPEP2	AE100027	18	112	TCACAGAG	A/G	ATCTCTCAG	608	AD008983	616	AD008983	79759	G	T	Intron13	Non-CDS	0			GA	616	NM_000623.1	
XPNPEP2	AE100029	21	291	GGTCTG	A/G	CTGCTGAA	607	AD008983	617	AD008983	79760	G	T	Intron13	Non-CDS	0			GA	617	NM_000623.1	
XPNPEP2	AE100030	21	291	GGTCTG	A/G	CTGCTGAA	608	AD008983	618	AD008983	79761	G	T	Intron13	Non-CDS	0			GA	618	NM_000623.1	
XPNPEP2	AE100032	22	144	GGTCTG	A/G	CTGCTGAA	609	AD008983	619	AD008983	79762	G	T	Intron13	Non-CDS	0			GA	619	NM_000623.1	
XPNPEP2	AE100031	7	789	ACAAAGTG	C/T	AGAGCGGCG	606	AD008983	620	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	620	NM_000623.1	
BNVHNF1	AE100810	7	1822	GTGAGGCT	C/T	GTGAGGCT	605	AD008983	621	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	621	NM_000623.1	
BNVHNF1	AE100812	7	1808	GTGAGGCT	C/T	GTGAGGCT	606	AD008983	622	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	622	NM_000623.1	
BNVHNF1	AE100813	7	1840	GTGAGGCT	C/T	GTGAGGCT	607	AD008983	623	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	623	NM_000623.1	
BNVHNF1	AE100814	7	1840	GTGAGGCT	C/T	GTGAGGCT	608	AD008983	624	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	624	NM_000623.1	
BNVHNF1	AE100815	7	1840	GTGAGGCT	C/T	GTGAGGCT	609	AD008983	625	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	625	NM_000623.1	
BNVHNF1	AE100816	7	1840	GTGAGGCT	C/T	GTGAGGCT	610	AD008983	626	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	626	NM_000623.1	
BNVHNF1	AE100817	7	1840	GTGAGGCT	C/T	GTGAGGCT	611	AD008983	627	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	627	NM_000623.1	
BNVHNF1	AE100818	7	1840	GTGAGGCT	C/T	GTGAGGCT	612	AD008983	628	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	628	NM_000623.1	
BNVHNF1	AE100819	7	1840	GTGAGGCT	C/T	GTGAGGCT	613	AD008983	629	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	629	NM_000623.1	
BNVHNF1	AE100820	7	1840	GTGAGGCT	C/T	GTGAGGCT	614	AD008983	630	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	630	NM_000623.1	
BNVHNF1	AE100821	7	1840	GTGAGGCT	C/T	GTGAGGCT	615	AD008983	631	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	631	NM_000623.1	
BNVHNF1	AE100822	7	1840	GTGAGGCT	C/T	GTGAGGCT	616	AD008983	632	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	632	NM_000623.1	
BNVHNF1	AE100823	7	1840	GTGAGGCT	C/T	GTGAGGCT	617	AD008983	633	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	633	NM_000623.1	
BNVHNF1	AE100824	7	1840	GTGAGGCT	C/T	GTGAGGCT	618	AD008983	634	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	634	NM_000623.1	
BNVHNF1	AE100825	7	1840	GTGAGGCT	C/T	GTGAGGCT	619	AD008983	635	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	635	NM_000623.1	
BNVHNF1	AE100826	7	1840	GTGAGGCT	C/T	GTGAGGCT	620	AD008983	636	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	636	NM_000623.1	
BNVHNF1	AE100827	7	1840	GTGAGGCT	C/T	GTGAGGCT	621	AD008983	637	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	637	NM_000623.1	
BNVHNF1	AE100828	7	1840	GTGAGGCT	C/T	GTGAGGCT	622	AD008983	638	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	638	NM_000623.1	
BNVHNF1	AE100829	7	1840	GTGAGGCT	C/T	GTGAGGCT	623	AD008983	639	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	639	NM_000623.1	
BNVHNF1	AE100830	7	1840	GTGAGGCT	C/T	GTGAGGCT	624	AD008983	640	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	640	NM_000623.1	
BNVHNF1	AE100831	7	1840	GTGAGGCT	C/T	GTGAGGCT	625	AD008983	641	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	641	NM_000623.1	
BNVHNF1	AE100832	7	1840	GTGAGGCT	C/T	GTGAGGCT	626	AD008983	642	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	642	NM_000623.1	
BNVHNF1	AE100833	7	1840	GTGAGGCT	C/T	GTGAGGCT	627	AD008983	643	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	643	NM_000623.1	
BNVHNF1	AE100834	7	1840	GTGAGGCT	C/T	GTGAGGCT	628	AD008983	644	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	644	NM_000623.1	
BNVHNF1	AE100835	7	1840	GTGAGGCT	C/T	GTGAGGCT	629	AD008983	645	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	645	NM_000623.1	
BNVHNF1	AE100836	7	1840	GTGAGGCT	C/T	GTGAGGCT	630	AD008983	646	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	646	NM_000623.1	
BNVHNF1	AE100837	7	1840	GTGAGGCT	C/T	GTGAGGCT	631	AD008983	647	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	647	NM_000623.1	
BNVHNF1	AE100838	7	1840	GTGAGGCT	C/T	GTGAGGCT	632	AD008983	648	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	648	NM_000623.1	
BNVHNF1	AE100839	7	1840	GTGAGGCT	C/T	GTGAGGCT	633	AD008983	649	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	649	NM_000623.1	
BNVHNF1	AE100840	7	1840	GTGAGGCT	C/T	GTGAGGCT	634	AD008983	650	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	650	NM_000623.1	
BNVHNF1	AE100841	7	1840	GTGAGGCT	C/T	GTGAGGCT	635	AD008983	651	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	651	NM_000623.1	
BNVHNF1	AE100842	7	1840	GTGAGGCT	C/T	GTGAGGCT	636	AD008983	652	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	652	NM_000623.1	
BNVHNF1	AE100843	7	1840	GTGAGGCT	C/T	GTGAGGCT	637	AD008983	653	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	653	NM_000623.1	
BNVHNF1	AE100844	7	1840	GTGAGGCT	C/T	GTGAGGCT	638	AD008983	654	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	654	NM_000623.1	
BNVHNF1	AE100845	7	1840	GTGAGGCT	C/T	GTGAGGCT	639	AD008983	655	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	655	NM_000623.1	
BNVHNF1	AE100846	7	1840	GTGAGGCT	C/T	GTGAGGCT	640	AD008983	656	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	656	NM_000623.1	
BNVHNF1	AE100847	7	1840	GTGAGGCT	C/T	GTGAGGCT	641	AD008983	657	AD008983	81149	T	C	Exon2	Non-CDS	0			GA	657	NM_000623.1	
BNVHNF1	AE100848	7	1840	GTGAGGCT	C/T	GTGAGGCT	642	AD008983	658	AD008983	81149	T										

[illegible]

[illegible]

GENE DESCRIPTION	HGNC ID	SNP ID	CONTIG_NUM	CONTIG_POS	REF_AA	ALT_AA	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN (SEQ ID NO.)	FLANK_SEQ REF (SEQ ID NO.)	FLANK_SEQ ALT (SEQ ID NO.)	REFSEQ_FLANK REF (SEQ ID NO.)
Amphipodopsin P (membrane-bound)	XPMP2P2	AE10041	1	127	P	P	Exon2	Silent	0	CCC	CCG	AABR53A.1	607	4	37	100	163
Bradykinin Receptor B1	BDKRB1	AE10341	6	307	R	Q	Exon2	Missense	0	CCG	CAG	NP_000701.1	317	8	60	123	186
Bradykinin Receptor B1	BDKRB1	AE10342	4	273	P	P	Exon2	Silent	0	CCG	CCA	NP_000701.1	41	10	61	124	187
Tachykinin Receptor 1	TACR1	AE10641	1	614	F	F	Exon1	Silent	1	TTT	TTC	NP_001049.1	111	16	81	144	207
Tachykinin Receptor 1	TACR1	AE10642	2	769	I	I	Exon2	Silent	1	ATC	ATA	NP_001049.1	154	18	82	145	208
Tachykinin Receptor 1	TACR1	AE10647	6	511	S	S	Exon5	Silent	1	TGG	TCA	NP_001049.1	378	20	87	150	213
C1 Esterase Inhibitor	C1INH	AE10543	5	366	S	S	Exon7	Silent	0	AGC	AGT	NP_000053.1	406	24	90	153	216
C1 Esterase Inhibitor	C1INH	AE10544	7	588	V	A	Exon3	Missense	0	GTT	GCT	NP_000053.1	58	26	91	154	217
C1 Esterase Inhibitor	C1INH	AE10555	7	897	A	G	Exon3	Missense	0	GCA	GGA	NP_000053.1	159	28	92	155	218
C1 Esterase Inhibitor	C1INH	AE10546	8	276	V	M	Exon8	Missense	0	GTG	ATG	NP_000053.1	480	30	93	156	219
Kallikrein 1 (renal/pancreas/submax)	KLK1	AE10741	1	153	K	E	Exon4	Missense	0	AAA	GAA	NP_002248.1	186	34	94	157	220
Kallikrein 1 (renal/pancreas/submax)	KLK1	AE10743	2	605	E	Q	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	36	96	159	222
Bradykinin Receptor B1	BDKRB1	AE10346	1	87	N	N	Exon3	Silent	0	AAC	AAT	NP_000701.1	114	556	579	611	643
Bradykinin Receptor B1	BDKRB1	AE10347	1	191	R	R	Exon3	Silent	0	AGG	AGA	NP_000701.1	152	558	580	612	644
Bradykinin Receptor B1	BDKRB1	AE10348	1	296	L	V	Exon3	Missense	0	CTG	GTG	NP_000701.1	191	560	581	613	645
Bradykinin Receptor B1	BDKRB1	AE10349	2	136	E	E	Exon3	Silent	0	GAG	GAA	NP_000701.1	233	562	582	614	646
Bradykinin Receptor B2	BDKRB2	AE104419	7	339	R	C	Exon2	Missense	1	CGT	TGT	NP_000614.1	14	564	584	616	648
Bradykinin Receptor B2	BDKRB2	AE104424	4	918	D	D	Exon3	Silent	1	GAT	GAC	NP_000614.1	311	566	586	621	653
Bradykinin Receptor B2	BDKRB2	AE104425	4	1046	G	E	Exon3	Missense	1	GCG	GAG	NP_000614.1	354	568	590	622	654
Angiotensin Converting Enzyme 2	ACE2	AE10947	15	241	N	N	Exon16	Silent	1	AAT	AAC	AA176220.1	690	843	891	833	665
Protease Inhibitor 4	P4	AE11042	2	526	F	F	Exon2	Silent	0	TTC	TTT	NP_000208.1	233	574	603	635	667
Protease Inhibitor 4	P4	AE11045	4	563	S	S	Exon1	Silent	0	AGT	AGC	NP_000208.1	199	576	606	638	670

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ACE2

DNA panel	Coriell Catalog #	Sample Description	XPMP2	BDRB1	BDRB2	TACR1	C1NH	KLK1	PI4	ACE2
Coriell 24 panel	NA14905	African American	X	X	X	X	X			
Coriell 24 panel	NA14922	African American	X	X	X	X	X			
Coriell 24 panel	NA14923	African American	X	X	X	X	X			
Coriell 24 panel	NA14924	African American	X	X	X	X	X			
Coriell 24 panel	NA14925	African American	X	X	X	X	X			
Coriell 24 panel	NA14932	African American	X	X	X	X	X			
Coriell 24 panel	NA14933	African American	X	X	X	X	X			
Coriell 24 panel	NA14934	African American	X	X	X	X	X			
Coriell 24 panel	NA 17201	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17202	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17203	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17204	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17205	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17206	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17207	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17208	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA00576	Chinese	X	X	X	X	X			
Coriell 24 panel	NA03433	Chinese	X	X	X	X	X			
Coriell 24 panel	NA06090	Chinese	X	X	X	X	X			
Coriell 24 panel	NA07426	Chinese	X	X	X	X	X			
Coriell 24 panel	NA02345b	Japanese	X	X	X	X	X			
Coriell 24 panel	NA11589	Japanese	X	X	X	X	X			
Coriell 24 panel	NA14819	Japanese	X	X	X	X	X			
Coriell 24 panel	NA04535	Japanese	X	X	X	X	X			
Coriell 24 panel	NA14672	African American	X	X	X	X	X			
Coriell 24 panel	NA14682	African American	X	X	X	X	X			
Coriell 24 panel	NA14683	African American	X	X	X	X	X			
Coriell 24 panel	NA14696	African American	X	X	X	X	X			
Coriell 24 panel	NA14698	African American	X	X	X	X	X			
Coriell 24 panel	NA14700	African American	X	X	X	X	X			
Coriell 24 panel	NA14704	African American	X	X	X	X	X			
Coriell 24 panel	NA1850	African American	X	X	X	X	X			
Coriell 24 panel	3382	African American	X	X	X	X	X			
Coriell 24 panel	3725	African American	X	X	X	X	X			
Coriell 24 panel	6865	African American	X	X	X	X	X			
Coriell 24 panel	7754	African American	X	X	X	X	X			
Coriell 24 panel	10251	African American	X	X	X	X	X			
Coriell 24 panel	10378	African American	X	X	X	X	X			
Coriell 24 panel	12931	African American	X	X	X	X	X			
Coriell 24 panel	13294	African American	X	X	X	X	X			
Coriell 24 panel	14439	African American	X	X	X	X	X			
Coriell 24 panel	14441	African American	X	X	X	X	X			
Coriell 24 panel	14454	African American	X	X	X	X	X			
Coriell 24 panel	14464	African American	X	X	X	X	X			

Table VII B

DNA panel	Coriell Catalog #	Sample Description	XPNEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 50/AA panel	14537	African American								
HD 50/AA panel	14583	African American								
HD 50/AA panel	14681	African American								
HD 50/AA panel	14687	African American								
HD 50/AA panel	14697	African American								
HD 50/AA panel	14699	African American								
HD 50/AA panel	14720	African American								
HD 50/AA panel	14746	African American								
HD 50/AA panel	14754	African American								
HD 50/AA panel	14755	African American								
HD 50/AA panel	14771	African American								
HD 50/AA panel	14772	African American								
HD 50/AA panel	14783	African American								
HD 50/AA panel	14826	African American								
HD 50/AA panel	14837	African American								
HD 50/AA panel	14862	African American								
HD 50/AA panel	14863	African American								
HD 50/AA panel	14864	African American								
HD 50/AA panel	14892	African American								
HD 50/AA panel	14893	African American								
HD 50/AA panel	14894	African American								
HD 50/AA panel	14895	African American								
HD 50/AA panel	14897	African American								
HD 50/AA panel	14900	African American								
HD 50/AA panel	14901	African American								
HD 50/AA panel	14903	African American								
HD 50/AA panel	14904	African American								
HD 50/AA panel	14905	African American								
HD 50/AA panel	14922	African American								
HD 50/AA panel	14923	African American								
HD 50/AA panel	14924	African American								
HD 50/AA panel	14925	African American								
HD 50/AA panel	14932	African American								
HD 50/AA panel	14933	African American								
HD 100/CAU panel	NA 17201	Caucasian								
HD 100/CAU panel	17202	Caucasian								
HD 100/CAU panel	17203	Caucasian								
HD 100/CAU panel	17204	Caucasian								
HD 100/CAU panel	17205	Caucasian								
HD 100/CAU panel	17206	Caucasian								
HD 100/CAU panel	17207	Caucasian								
HD 100/CAU panel	17208	Caucasian								
HD 100/CAU panel	17209	Caucasian								
HD 100/CAU panel	17210	Caucasian								

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Table VIIC

DNA panel	Coriell Catalog #	Sample Description	XPBPEP2	BKCRB1	BKCRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17211	Caucasian								
HD 100 CAU panel	17212	Caucasian								
HD 100 CAU panel	17213	Caucasian								
HD 100 CAU panel	17214	Caucasian								
HD 100 CAU panel	17215	Caucasian								
HD 100 CAU panel	17216	Caucasian								
HD 100 CAU panel	17217	Caucasian								
HD 100 CAU panel	17218	Caucasian								
HD 100 CAU panel	17219	Caucasian								
HD 100 CAU panel	17220	Caucasian								
HD 100 CAU panel	17221	Caucasian								
HD 100 CAU panel	17222	Caucasian								
HD 100 CAU panel	17223	Caucasian								
HD 100 CAU panel	17224	Caucasian								
HD 100 CAU panel	17225	Caucasian								
HD 100 CAU panel	17226	Caucasian								
HD 100 CAU panel	17227	Caucasian								
HD 100 CAU panel	17228	Caucasian								
HD 100 CAU panel	17229	Caucasian								
HD 100 CAU panel	17230	Caucasian								
HD 100 CAU panel	17231	Caucasian								
HD 100 CAU panel	17232	Caucasian								
HD 100 CAU panel	17233	Caucasian								
HD 100 CAU panel	17234	Caucasian								
HD 100 CAU panel	17235	Caucasian								
HD 100 CAU panel	17236	Caucasian								
HD 100 CAU panel	17237	Caucasian								
HD 100 CAU panel	17238	Caucasian								
HD 100 CAU panel	17239	Caucasian								
HD 100 CAU panel	17240	Caucasian								
HD 100 CAU panel	17241	Caucasian								
HD 100 CAU panel	17242	Caucasian								
HD 100 CAU panel	17243	Caucasian								
HD 100 CAU panel	17244	Caucasian								
HD 100 CAU panel	17245	Caucasian								
HD 100 CAU panel	17246	Caucasian								
HD 100 CAU panel	17247	Caucasian								
HD 100 CAU panel	17248	Caucasian								
HD 100 CAU panel	17249	Caucasian								
HD 100 CAU panel	17250	Caucasian								
HD 100 CAU panel	17251	Caucasian								
HD 100 CAU panel	17252	Caucasian								
HD 100 CAU panel	17253	Caucasian								
HD 100 CAU panel	17254	Caucasian								

GENE DESCRIPTION	HGNC ID	SNP ID	EXON	REVCOMP	PCR Amplicon Name	Target Name	PCR Left primer	PCR Left primer (SEQ ID NO:)	PCR Right primer	PCR Right primer (SEQ ID NO:)
Antropodiplosa P (membrane-bound)	XPNEP2	AE10051	Exon20	0	AE10051p7b	XPNEP2_X20a	AGTGTCTCTCTCTCTCTCTCT	287	TATTCATCTACCTGGGGTTGGG	360
Antropodiplosa P (membrane-bound)	XPNEP2	AE10052	Intron3	0	AE10052p10	XPNEP2_X3a	CAGCCAGGACATCTTAATCTA	288	TCTCTACTTCCCTGCTTGG	361
Antropodiplosa P (membrane-bound)	XPNEP2	AE10053	Intron15	0	AE10053p58	XPNEP2_X15a	TAGCTGTCTCTCTCTCTCTCT	289	ATAGATGAGGCTCAGCTTGG	362
Antropodiplosa P (membrane-bound)	XPNEP2	AE10054	Intron15	0	AE10054p58	XPNEP2_X15a	TAGCTGTCTCTCTCTCTCTCT	300	ATAGATGAGGCTCAGCTTGG	363
Antropodiplosa P (membrane-bound)	XPNEP2	AE10055	Intron1	0	AE10055p2	XPNEP2_X1a	TGATGAGACGAGCTTGTTGG	301	ACAGAAAAGAGAGCTGGGG	364
Antropodiplosa P (membrane-bound)	XPNEP2	AE10056	Intron7	0	AE10056p26	XPNEP2_X7a	CGAGGCTGGGCATACATG	302	GGCCTGAAATCTGCAATT	365
Antropodiplosa P (membrane-bound)	XPNEP2	AE10057	Intron7	0	AE10057p26	XPNEP2_X7a	CGAGGCTGGGCATACATG	303	GGCCTGAAATCTGCAATT	366
Antropodiplosa P (membrane-bound)	XPNEP2	AE10058	Intron10	0	AE10058p38	XPNEP2_X10a	CTCTCTTTGACCTTCAGGAAC	304	CGTGTCTCTCTCTCTCTCT	367
Antropodiplosa P (membrane-bound)	XPNEP2	AE10059	Intron10	0	AE10059p38	XPNEP2_X10a	CTCTCTTTGACCTTCAGGAAC	305	CGTGTCTCTCTCTCTCTCT	368
Antropodiplosa P (membrane-bound)	XPNEP2	AE10060	Intron7	0	AE10060p50	XPNEP2_X7a	TAATGACAGCTCAGGGCTTG	306	GGCCTGAAATCTGCAATT	369
Antropodiplosa P (membrane-bound)	XPNEP2	AE10061	Intron13	0	AE10061p50	XPNEP2_X13a	TAATGACAGCTCAGGGCTTG	307	CAGGCTCAGAGGCTTTTCAIT	370
Antropodiplosa P (membrane-bound)	XPNEP2	AE10062	Intron13	0	AE10062p50	XPNEP2_X13a	TAATGACAGCTCAGGGCTTG	308	CAGGCTCAGAGGCTTTTCAIT	371
Antropodiplosa P (membrane-bound)	XPNEP2	AE10063	Intron13	0	AE10063p50	XPNEP2_X13a	TAATGACAGCTCAGGGCTTG	309	CAGGCTCAGAGGCTTTTCAIT	372
Antropodiplosa P (membrane-bound)	XPNEP2	AE10064	Exon1	0	AE10064p2	XPNEP2_X1a	GGACTATGGTGAAGCTGGAG	310	ACAGAAAAGAGAGCTGGGG	373
Antropodiplosa P (membrane-bound)	XPNEP2	AE10065	Exon21	0	AE10065p68	XPNEP2_X21a	GGAGCTCCAGACTTCTCTGTT	311	ACAGAAAAGAGAGCTGGGG	374
Antropodiplosa P (membrane-bound)	XPNEP2	AE10066	Exon21	0	AE10066p68	XPNEP2_X21a	GGAGCTCCAGACTTCTCTGTT	312	TAGGATGATGGGTTCATG	375
Antropodiplosa P (membrane-bound)	XPNEP2	AE10067	Intron17	0	AE10067p68	XPNEP2_X17a	CGCTCTCTTCTAGGCACTTC	313	CTGCTGGCAATCTCTCACTAC	376
Antropodiplosa P (membrane-bound)	XPNEP2	AE10068	Intron17	0	AE10068p68	XPNEP2_X17a	CGCTCTCTTCTAGGCACTTC	314	CTGCTGGCAATCTCTCACTAC	377
Antropodiplosa P (membrane-bound)	XPNEP2	AE10069	Intron15	0	AE10069p58	XPNEP2_X15a	TAGCTGTCTCTCTCTCTCTCT	315	ATAGATGAGGCTCAGCTTGG	378
Antropodiplosa P (membrane-bound)	XPNEP2	AE10070	Intron21	0	AE10070p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	316	CAAGAAGGCTGTGTCTCTG	379
Antropodiplosa P (membrane-bound)	XPNEP2	AE10071	Exon21	0	AE10071p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	317	CAAGAAGGCTGTGTCTCTG	380
Antropodiplosa P (membrane-bound)	XPNEP2	AE10072	Exon21	0	AE10072p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	318	CAAGAAGGCTGTGTCTCTG	381
Antropodiplosa P (membrane-bound)	XPNEP2	AE10073	Exon21	0	AE10073p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	319	CAAGAAGGCTGTGTCTCTG	382
Antropodiplosa P (membrane-bound)	XPNEP2	AE10074	Exon21	0	AE10074p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	320	CAAGAAGGCTGTGTCTCTG	383
Antropodiplosa P (membrane-bound)	XPNEP2	AE10075	Exon21	0	AE10075p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	321	CAAGAAGGCTGTGTCTCTG	384
Antropodiplosa P (membrane-bound)	XPNEP2	AE10076	Exon21	0	AE10076p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	322	CAAGAAGGCTGTGTCTCTG	385
Antropodiplosa P (membrane-bound)	XPNEP2	AE10077	Exon21	0	AE10077p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	323	CAAGAAGGCTGTGTCTCTG	386
Antropodiplosa P (membrane-bound)	XPNEP2	AE10078	Exon21	0	AE10078p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	324	CAAGAAGGCTGTGTCTCTG	387
Antropodiplosa P (membrane-bound)	XPNEP2	AE10079	Exon21	0	AE10079p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	325	CAAGAAGGCTGTGTCTCTG	388
Antropodiplosa P (membrane-bound)	XPNEP2	AE10080	Exon21	0	AE10080p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	326	CAAGAAGGCTGTGTCTCTG	389
Antropodiplosa P (membrane-bound)	XPNEP2	AE10081	Exon21	0	AE10081p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	327	CAAGAAGGCTGTGTCTCTG	390
Antropodiplosa P (membrane-bound)	XPNEP2	AE10082	Exon21	0	AE10082p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	328	CAAGAAGGCTGTGTCTCTG	391
Antropodiplosa P (membrane-bound)	XPNEP2	AE10083	Exon21	0	AE10083p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	329	CAAGAAGGCTGTGTCTCTG	392
Antropodiplosa P (membrane-bound)	XPNEP2	AE10084	Exon21	0	AE10084p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	330	CAAGAAGGCTGTGTCTCTG	393
Antropodiplosa P (membrane-bound)	XPNEP2	AE10085	Exon21	0	AE10085p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	331	CAAGAAGGCTGTGTCTCTG	394
Antropodiplosa P (membrane-bound)	XPNEP2	AE10086	Exon21	0	AE10086p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	332	CAAGAAGGCTGTGTCTCTG	395
Antropodiplosa P (membrane-bound)	XPNEP2	AE10087	Exon21	0	AE10087p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	333	CAAGAAGGCTGTGTCTCTG	396
Antropodiplosa P (membrane-bound)	XPNEP2	AE10088	Exon21	0	AE10088p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	334	CAAGAAGGCTGTGTCTCTG	397
Antropodiplosa P (membrane-bound)	XPNEP2	AE10089	Exon21	0	AE10089p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	335	CAAGAAGGCTGTGTCTCTG	398
Antropodiplosa P (membrane-bound)	XPNEP2	AE10090	Exon21	0	AE10090p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	336	CAAGAAGGCTGTGTCTCTG	399
Antropodiplosa P (membrane-bound)	XPNEP2	AE10091	Exon21	0	AE10091p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	337	CAAGAAGGCTGTGTCTCTG	400
Antropodiplosa P (membrane-bound)	XPNEP2	AE10092	Exon21	0	AE10092p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	338	CAAGAAGGCTGTGTCTCTG	401
Antropodiplosa P (membrane-bound)	XPNEP2	AE10093	Exon21	0	AE10093p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	339	CAAGAAGGCTGTGTCTCTG	402
Antropodiplosa P (membrane-bound)	XPNEP2	AE10094	Exon21	0	AE10094p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	340	CAAGAAGGCTGTGTCTCTG	403
Antropodiplosa P (membrane-bound)	XPNEP2	AE10095	Exon21	0	AE10095p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	341	CAAGAAGGCTGTGTCTCTG	404
Antropodiplosa P (membrane-bound)	XPNEP2	AE10096	Exon21	0	AE10096p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	342	CAAGAAGGCTGTGTCTCTG	405
Antropodiplosa P (membrane-bound)	XPNEP2	AE10097	Exon21	0	AE10097p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	343	CAAGAAGGCTGTGTCTCTG	406
Antropodiplosa P (membrane-bound)	XPNEP2	AE10098	Exon21	0	AE10098p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	344	CAAGAAGGCTGTGTCTCTG	407
Antropodiplosa P (membrane-bound)	XPNEP2	AE10099	Exon21	0	AE10099p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	345	CAAGAAGGCTGTGTCTCTG	408
Antropodiplosa P (membrane-bound)	XPNEP2	AE10100	Exon21	0	AE10100p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	346	CAAGAAGGCTGTGTCTCTG	409
Antropodiplosa P (membrane-bound)	XPNEP2	AE10101	Exon21	0	AE10101p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	347	CAAGAAGGCTGTGTCTCTG	410
Antropodiplosa P (membrane-bound)	XPNEP2	AE10102	Exon21	0	AE10102p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	348	CAAGAAGGCTGTGTCTCTG	411
Antropodiplosa P (membrane-bound)	XPNEP2	AE10103	Exon21	0	AE10103p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	349	CAAGAAGGCTGTGTCTCTG	412
Antropodiplosa P (membrane-bound)	XPNEP2	AE10104	Exon21	0	AE10104p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	350	CAAGAAGGCTGTGTCTCTG	413
Antropodiplosa P (membrane-bound)	XPNEP2	AE10105	Exon21	0	AE10105p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	351	CAAGAAGGCTGTGTCTCTG	414
Antropodiplosa P (membrane-bound)	XPNEP2	AE10106	Exon21	0	AE10106p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	352	CAAGAAGGCTGTGTCTCTG	415
Antropodiplosa P (membrane-bound)	XPNEP2	AE10107	Exon21	0	AE10107p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	353	CAAGAAGGCTGTGTCTCTG	416
Antropodiplosa P (membrane-bound)	XPNEP2	AE10108	Exon21	0	AE10108p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	354	CAAGAAGGCTGTGTCTCTG	417
Antropodiplosa P (membrane-bound)	XPNEP2	AE10109	Exon21	0	AE10109p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	355	CAAGAAGGCTGTGTCTCTG	418
Antropodiplosa P (membrane-bound)	XPNEP2	AE10110	Exon21	0	AE10110p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	356	CAAGAAGGCTGTGTCTCTG	419
Antropodiplosa P (membrane-bound)	XPNEP2	AE10111	Exon21	0	AE10111p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	357	CAAGAAGGCTGTGTCTCTG	420
Antropodiplosa P (membrane-bound)	XPNEP2	AE10112	Exon21	0	AE10112p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	358	CAAGAAGGCTGTGTCTCTG	421
Antropodiplosa P (membrane-bound)	XPNEP2	AE10113	Exon21	0	AE10113p82	XPNEP2_X21.1a	GGACTATGGTGAAGCTGGAG	359	CAAGAAGGCTGTGTCTCTG	422

Table VIII (2 of 2)

GENE DESCRIPTION	HMC ID	SNP ID	EXON	REWCOMP	PCR Amplicon Name	Target Name	PCR Left primer (SEQ ID NO.)	PCR Right primer (SEQ ID NO.)	PCR Right primer (SEQ ID NO.)
Bradykinin Receptor B1	BDKRB1	AE10356	Exon3	0	AE10356p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTCG	739
Bradykinin Receptor B1	BDKRB1	AE10357	Exon3	0	AE10356p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTCG	740
Bradykinin Receptor B1	BDKRB1	AE10358	Exon3	0	AE10356p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTCG	741
Bradykinin Receptor B1	BDKRB1	AE10359	Exon3	0	AE10356p10	U48231_X2.12a	GCCTCTGATCTGGTGTTC	CTGTGGTCTGCTATCTCTCG	742
Bradykinin Receptor B2	BDKRB2	AE10418	Intron1 or Exon2	1	AE10418p56	BDKRB2_X3.5a	CACCTTGCAGGAAATGTTGGAG	AAGAACCAAGCAAGCTTCTGGT	743
Bradykinin Receptor B2	BDKRB2	AE10419	Exon2	0	AE10418p56	BDKRB2_X3.5a	GGCAGGCGAGGAAATAGTCT	AGATCCAGACAGAGAGAGAGG	744
Bradykinin Receptor B2	BDKRB2	AE10420	Exon2	1	AE10418p56	BDKRB2_X3.5a	GGCAGGCGAGGAAATAGTCT	AGATCCAGACAGAGAGAGAGG	745
Bradykinin Receptor B2	BDKRB2	AE10421	5' Flank	1	AE10418p56	BDKRB2_X3.5a	CTGGGATTTCTTTGATGGCA	AGAGCTACAGCAAGTTCACA	746
Bradykinin Receptor B2	BDKRB2	AE10422	5' Flank	1	AE10418p56	BDKRB2_X3.5a	CTGGGATTTCTTTGATGGCA	AGAGCTACAGCAAGTTCACA	747
Bradykinin Receptor B2	BDKRB2	AE10423	5' Flank	1	AE10418p56	BDKRB2_X3.5a	CTGGGATTTCTTTGATGGCA	AGAGCTACAGCAAGTTCACA	748
Bradykinin Receptor B2	BDKRB2	AE10424	5' Flank	1	AE10418p56	BDKRB2_X3.5a	CTGGGATTTCTTTGATGGCA	AGAGCTACAGCAAGTTCACA	749
Bradykinin Receptor B2	BDKRB2	AE10425	Exon3	1	AE10418p56	BDKRB2_X3.5a	GGCAGGCGAGGAAATAGTCT	AGATCCAGACAGAGAGAGAGG	750
Bradykinin Receptor B2	BDKRB2	AE10426	Exon3	1	AE10418p56	BDKRB2_X3.5a	GGCAGGCGAGGAAATAGTCT	AGATCCAGACAGAGAGAGAGG	751
Bradykinin Receptor B2	BDKRB2	AE10427	Exon3	1	AE10418p56	BDKRB2_X3.5a	GACCTCTGTCATCAGTGA	GGCTGTGCTCAAGTTTGTGTG	752
Bradykinin Receptor B2	BDKRB2	AE10428	Exon3	1	AE10418p56	BDKRB2_X3.5a	TOCCAGTTCAGTCTGCTAAT	GGTGTGATGACAGCAGAGAG	753
Bradykinin Receptor B2	BDKRB2	AE10429	Exon3	1	AE10418p56	BDKRB2_X3.5a	GGCAGCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	754
Angiotensin Converting Enzyme 2	ACE2	AE10951	Intron14	1	AE10951p28	ACE2_X14a	TTTAAACCCCAAGCCCAAGG	TTTCTGCTTTTCCAAAGCC	755
Angiotensin Converting Enzyme 2	ACE2	AE10952	Intron12	1	AE10951p30	ACE2_X13a	CACCATAGCAGAGAAAGAGCA	GCCAGTCAAGAGAGAAAGCC	756
Angiotensin Converting Enzyme 2	ACE2	AE10953	Intron13	1	AE10951p30	ACE2_X13a	CACCATAGCAGAGAAAGAGCA	GCCAGTCAAGAGAGAAAGCC	757
Angiotensin Converting Enzyme 2	ACE2	AE10954	Intron3	1	AE10951p30	ACE2_X13a	GTAAGGTTGGCAGACATCAGG	AAAAATCATGTGTCTCAAGGA	758
Angiotensin Converting Enzyme 2	ACE2	AE10955	Intron2	1	AE10951p30	ACE2_X13a	GTAAGGTTGGCAGACATCAGG	AAAAATCATGTGTCTCAAGGA	759
Angiotensin Converting Enzyme 2	ACE2	AE10956	Intron16	1	AE10951p30	ACE2_X13a	GTAAGGTTGGCAGACATCAGG	AAAAATCATGTGTCTCAAGGA	760
Angiotensin Converting Enzyme 2	ACE2	AE10957	Exon16	1	AE10951p30	ACE2_X13a	CTGTGGGATCTCTGTGGAAAT	CAATACATCTCTCTCAATTTGC	761
Protease Inhibitor 4	PI4	AE11081	Intron1	0	AE11081p22	PI4_X2a	GGACATCTGATGGGCTCAT	TGGGGGACATGCTTCTCATAG	762
Protease Inhibitor 4	PI4	AE11082	Exon2	0	AE11081p22	PI4_X2a	GGACATCTGATGGGCTCAT	TGGGGGACATGCTTCTCATAG	763
Protease Inhibitor 4	PI4	AE11083	Intron2	0	AE11081p22	PI4_X2a	GGACATCTGATGGGCTCAT	TGGGGGACATGCTTCTCATAG	764
Protease Inhibitor 4	PI4	AE11084	Intron2	0	AE11081p22	PI4_X2a	GGACATCTGATGGGCTCAT	TGGGGGACATGCTTCTCATAG	765
Protease Inhibitor 4	PI4	AE11085	Intron2	0	AE11081p22	PI4_X2a	GGACATCTGATGGGCTCAT	TGGGGGACATGCTTCTCATAG	766
Protease Inhibitor 4	PI4	AE11086	5' Flank	0	AE11085p6	PI4_X1.12a	TAGAGCTTTTGGGCTTGACA	TGAGCTGTGCAGACAGCTAGA	767
Protease Inhibitor 4	PI4	AE11087	5' Flank	0	AE11085p6	PI4_X1.12a	TAGAGCTTTTGGGCTTGACA	TGAGCTGTGCAGACAGCTAGA	768
Protease Inhibitor 4	PI4	AE11088	5' Flank	0	AE11085p6	PI4_X1.12a	TAGAGCTTTTGGGCTTGACA	TGAGCTGTGCAGACAGCTAGA	769
Protease Inhibitor 4	PI4	AE11089	5' Flank	0	AE11085p6	PI4_X1.12a	TAGAGCTTTTGGGCTTGACA	TGAGCTGTGCAGACAGCTAGA	770
Antipeptidase P (membrane-bound)	XPNPEP2	AE100524	Intron11	0	AE100524p46	XPNPEP2_X12a	TTTTCACAGCTCCACATCTCTG	TGGAGTGTCTCTGCTCTCAG	988
Antipeptidase P (membrane-bound)	XPNPEP2	AE100525	Intron13	0	AE100524p46	XPNPEP2_X12a	TTTTCACAGCTCCACATCTCTG	TGGAGTGTCTCTGCTCTCAG	989
Antipeptidase P (membrane-bound)	XPNPEP2	AE100526	Intron13	0	AE100524p46	XPNPEP2_X12a	TTTTCACAGCTCCACATCTCTG	TGGAGTGTCTCTGCTCTCAG	990
Antipeptidase P (membrane-bound)	XPNPEP2	AE100527	Intron7	0	AE100524p46	XPNPEP2_X12a	TTTTCACAGCTCCACATCTCTG	TGGAGTGTCTCTGCTCTCAG	991
Antipeptidase P (membrane-bound)	XPNPEP2	AE100528	Exon21	0	AE100524p46	XPNPEP2_X12a	TTTTCACAGCTCCACATCTCTG	TGGAGTGTCTCTGCTCTCAG	992
Antipeptidase P (membrane-bound)	XPNPEP2	AE100529	Exon21	0	AE100524p46	XPNPEP2_X12a	TTTTCACAGCTCCACATCTCTG	TGGAGTGTCTCTGCTCTCAG	993
Antipeptidase P (membrane-bound)	XPNPEP2	AE100530	Exon6	0	AE100524p46	XPNPEP2_X12a	TTTTCACAGCTCCACATCTCTG	TGGAGTGTCTCTGCTCTCAG	994
Bradykinin Receptor B1	BDKRB1	AE103510	Exon3	0	AE103525p28	U48231_X2.12a	GAGATCTCTTCCAGAGGCTC	TGCACGCTCTCACTATACCT	995
Bradykinin Receptor B1	BDKRB1	AE103511	Exon3	0	AE103525p28	U48231_X2.12a	GAGATCTCTTCCAGAGGCTC	TGCACGCTCTCACTATACCT	996
Bradykinin Receptor B1	BDKRB1	AE103512	Exon3	0	AE103525p28	U48231_X2.12a	GAGATCTCTTCCAGAGGCTC	TGCACGCTCTCACTATACCT	997
Bradykinin Receptor B1	BDKRB1	AE103513	Exon3	0	AE103525p28	U48231_X2.12a	GAGATCTCTTCCAGAGGCTC	TGCACGCTCTCACTATACCT	998
Bradykinin Receptor B1	BDKRB1	AE103514	Exon3	0	AE103525p28	U48231_X2.12a	GAGATCTCTTCCAGAGGCTC	TGCACGCTCTCACTATACCT	999
Bradykinin Receptor B2	BDKRB2	AE104330	Exon3	1	AE104330p24	BDKRB2_X3.12a	GCGACCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	1000
Bradykinin Receptor B2	BDKRB2	AE104331	Exon3	1	AE104330p24	BDKRB2_X3.12a	GCGACCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	1001
Bradykinin Receptor B2	BDKRB2	AE104332	Intron1	1	AE104330p24	BDKRB2_X3.12a	GCGACCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	1002
Bradykinin Receptor B2	BDKRB2	AE104333	Intron1	1	AE104330p24	BDKRB2_X3.12a	GCGACCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	1003
Bradykinin Receptor B2	BDKRB2	AE104334	Exon3	1	AE104330p24	BDKRB2_X3.12a	GCGACCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	1004
Bradykinin Receptor B2	BDKRB2	AE104335	Exon3	1	AE104330p24	BDKRB2_X3.12a	GCGACCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	1005
Bradykinin Receptor B2	BDKRB2	AE104336	Exon3	1	AE104330p24	BDKRB2_X3.12a	GCGACCTTCCAAATAACCAAT	GGTGTGATGACAGCAGAGAG	1006
Protease Inhibitor 4	PI4	AE110810	Exon4	0	AE110810p30	PI4_X4a	ATTTCTGAGCTTCCAGAGTCTT	CTTTCCAGAGGCGCAACTT	1007
Protease Inhibitor 4	PI4	AE110811	Exon4	0	AE110810p30	PI4_X4a	ATTTCTGAGCTTCCAGAGTCTT	CTTTCCAGAGGCGCAACTT	1008
Protease Inhibitor 4	PI4	AE110812	5' Flank	0	AE110810p30	PI4_X4a	ATTTCTGAGCTTCCAGAGTCTT	CTTTCCAGAGGCGCAACTT	1009
Tachykinin Receptor 1	TACR1	AE10656	Intron4	1	AE10656p10	TACR1_X4a	ATTTCTGAGCTTCCAGAGTCTT	CTTTCCAGAGGCGCAACTT	1010
Tachykinin Receptor 1	TACR1	AE10657	Intron3	1	AE10656p10	TACR1_X4a	ATTTCTGAGCTTCCAGAGTCTT	CTTTCCAGAGGCGCAACTT	1011
Angiotensin Converting Enzyme 2	ACE2	AE10958	Intron13	1	AE10958p30	ACE2_X13a	CACCATAGCAGAGAAAGAGCA	GCCAGTCAAGAGAGAAAGCC	1012
Angiotensin Converting Enzyme 2	ACE2	AE10959	Intron6	1	AE10958p30	ACE2_X13a	CACCATAGCAGAGAAAGAGCA	GCCAGTCAAGAGAGAAAGCC	1013

Table IX (1 of 2)

GENE DESCRIPTION	HGNC ID	SNP ID	EXON	REVCOMP	Target Name	Forward sequencing primer	Forward seq name	Forward sequencing primer (SEQ ID NO.)	Reverse sequencing primer	Reverse seq name
Antihypertensive P (membrane-bound)	XPMPF2	AE10061	Intn20	0	XPMPF2_X20a	AGTCTGCTCTGCTCTGCTACT	AE100678	AGCTTGGTCTCTGCTGGAAGT	AE100680	429
	XPMPF2	AE10062	Intn20	0	XPMPF2_X20a	CAGTAACTATCTGCTTGGCAGC	AE100679	TCTGTGTTTGTGCTCTGCTGAG	AE100681	430
	XPMPF2	AE10063	Intn15	0	XPMPF2_X15a	CACCTTGTGGAAAGCAGCAGCA	AE100680	TCTCAGTGGCTGCTGCTGCTG	AE100682	431
	XPMPF2	AE10064	Intn15	0	XPMPF2_X15a	CACCTTGTGGAAAGCAGCAGCA	AE100681	TCTCAGTGGCTGCTGCTGCTG	AE100683	432
	XPMPF2	AE10065	Intn17	0	XPMPF2_X17a	CCTGTGCTCTGAGATCTTGGTA	AE100682	TGAGTGTCAAGCTTGGCTTCTG	AE100684	433
	XPMPF2	AE10066	Intn17	0	XPMPF2_X17a	CCTGTGCTCTGAGATCTTGGTA	AE100683	TGAGTGTCAAGCTTGGCTTCTG	AE100685	434
	XPMPF2	AE10067	Intn17	0	XPMPF2_X17a	CCTGTGCTCTGAGATCTTGGTA	AE100684	TGAGTGTCAAGCTTGGCTTCTG	AE100686	435
	XPMPF2	AE10068	Intn17	0	XPMPF2_X17a	CCTGTGCTCTGAGATCTTGGTA	AE100685	TGAGTGTCAAGCTTGGCTTCTG	AE100687	436
	XPMPF2	AE10069	Intn17	0	XPMPF2_X17a	CCTGTGCTCTGAGATCTTGGTA	AE100686	TGAGTGTCAAGCTTGGCTTCTG	AE100688	437
	XPMPF2	AE10070	Intn17	0	XPMPF2_X17a	CCTGTGCTCTGAGATCTTGGTA	AE100687	TGAGTGTCAAGCTTGGCTTCTG	AE100689	438
Antihypertensive P (membrane-bound)	XPMPF2	AE10071	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100688	TGAGTGTCAAGCTTGGCTTCTG	AE100690	439
	XPMPF2	AE10072	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100689	TGAGTGTCAAGCTTGGCTTCTG	AE100691	440
	XPMPF2	AE10073	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100690	TGAGTGTCAAGCTTGGCTTCTG	AE100692	441
	XPMPF2	AE10074	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100691	TGAGTGTCAAGCTTGGCTTCTG	AE100693	442
	XPMPF2	AE10075	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100692	TGAGTGTCAAGCTTGGCTTCTG	AE100694	443
	XPMPF2	AE10076	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100693	TGAGTGTCAAGCTTGGCTTCTG	AE100695	444
	XPMPF2	AE10077	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100694	TGAGTGTCAAGCTTGGCTTCTG	AE100696	445
	XPMPF2	AE10078	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100695	TGAGTGTCAAGCTTGGCTTCTG	AE100697	446
	XPMPF2	AE10079	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100696	TGAGTGTCAAGCTTGGCTTCTG	AE100698	447
	XPMPF2	AE10080	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100697	TGAGTGTCAAGCTTGGCTTCTG	AE100699	448
Antihypertensive P (membrane-bound)	XPMPF2	AE10081	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100698	TGAGTGTCAAGCTTGGCTTCTG	AE100700	449
	XPMPF2	AE10082	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100699	TGAGTGTCAAGCTTGGCTTCTG	AE100701	450
	XPMPF2	AE10083	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100700	TGAGTGTCAAGCTTGGCTTCTG	AE100702	451
	XPMPF2	AE10084	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100701	TGAGTGTCAAGCTTGGCTTCTG	AE100703	452
	XPMPF2	AE10085	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100702	TGAGTGTCAAGCTTGGCTTCTG	AE100704	453
	XPMPF2	AE10086	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100703	TGAGTGTCAAGCTTGGCTTCTG	AE100705	454
	XPMPF2	AE10087	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100704	TGAGTGTCAAGCTTGGCTTCTG	AE100706	455
	XPMPF2	AE10088	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100705	TGAGTGTCAAGCTTGGCTTCTG	AE100707	456
	XPMPF2	AE10089	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100706	TGAGTGTCAAGCTTGGCTTCTG	AE100708	457
	XPMPF2	AE10090	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100707	TGAGTGTCAAGCTTGGCTTCTG	AE100709	458
Antihypertensive P (membrane-bound)	XPMPF2	AE10091	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100708	TGAGTGTCAAGCTTGGCTTCTG	AE100710	459
	XPMPF2	AE10092	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100709	TGAGTGTCAAGCTTGGCTTCTG	AE100711	460
	XPMPF2	AE10093	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100710	TGAGTGTCAAGCTTGGCTTCTG	AE100712	461
	XPMPF2	AE10094	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100711	TGAGTGTCAAGCTTGGCTTCTG	AE100713	462
	XPMPF2	AE10095	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100712	TGAGTGTCAAGCTTGGCTTCTG	AE100714	463
	XPMPF2	AE10096	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100713	TGAGTGTCAAGCTTGGCTTCTG	AE100715	464
	XPMPF2	AE10097	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100714	TGAGTGTCAAGCTTGGCTTCTG	AE100716	465
	XPMPF2	AE10098	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100715	TGAGTGTCAAGCTTGGCTTCTG	AE100717	466
	XPMPF2	AE10099	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100716	TGAGTGTCAAGCTTGGCTTCTG	AE100718	467
	XPMPF2	AE10100	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100717	TGAGTGTCAAGCTTGGCTTCTG	AE100719	468
Antihypertensive P (membrane-bound)	XPMPF2	AE10101	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100718	TGAGTGTCAAGCTTGGCTTCTG	AE100720	469
	XPMPF2	AE10102	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100719	TGAGTGTCAAGCTTGGCTTCTG	AE100721	470
	XPMPF2	AE10103	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100720	TGAGTGTCAAGCTTGGCTTCTG	AE100722	471
	XPMPF2	AE10104	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100721	TGAGTGTCAAGCTTGGCTTCTG	AE100723	472
	XPMPF2	AE10105	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100722	TGAGTGTCAAGCTTGGCTTCTG	AE100724	473
	XPMPF2	AE10106	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100723	TGAGTGTCAAGCTTGGCTTCTG	AE100725	474
	XPMPF2	AE10107	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100724	TGAGTGTCAAGCTTGGCTTCTG	AE100726	475
	XPMPF2	AE10108	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100725	TGAGTGTCAAGCTTGGCTTCTG	AE100727	476
	XPMPF2	AE10109	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100726	TGAGTGTCAAGCTTGGCTTCTG	AE100728	477
	XPMPF2	AE10110	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100727	TGAGTGTCAAGCTTGGCTTCTG	AE100729	478
Antihypertensive P (membrane-bound)	XPMPF2	AE10111	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100728	TGAGTGTCAAGCTTGGCTTCTG	AE100730	479
	XPMPF2	AE10112	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100729	TGAGTGTCAAGCTTGGCTTCTG	AE100731	480
	XPMPF2	AE10113	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100730	TGAGTGTCAAGCTTGGCTTCTG	AE100732	481
	XPMPF2	AE10114	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100731	TGAGTGTCAAGCTTGGCTTCTG	AE100733	482
	XPMPF2	AE10115	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100732	TGAGTGTCAAGCTTGGCTTCTG	AE100734	483
	XPMPF2	AE10116	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100733	TGAGTGTCAAGCTTGGCTTCTG	AE100735	484
	XPMPF2	AE10117	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100734	TGAGTGTCAAGCTTGGCTTCTG	AE100736	485
	XPMPF2	AE10118	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100735	TGAGTGTCAAGCTTGGCTTCTG	AE100737	486
	XPMPF2	AE10119	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100736	TGAGTGTCAAGCTTGGCTTCTG	AE100738	487
	XPMPF2	AE10120	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100737	TGAGTGTCAAGCTTGGCTTCTG	AE100739	488
Antihypertensive P (membrane-bound)	XPMPF2	AE10121	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100738	TGAGTGTCAAGCTTGGCTTCTG	AE100740	489
	XPMPF2	AE10122	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100739	TGAGTGTCAAGCTTGGCTTCTG	AE100741	490
	XPMPF2	AE10123	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100740	TGAGTGTCAAGCTTGGCTTCTG	AE100742	491
	XPMPF2	AE10124	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100741	TGAGTGTCAAGCTTGGCTTCTG	AE100743	492
	XPMPF2	AE10125	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100742	TGAGTGTCAAGCTTGGCTTCTG	AE100744	493
	XPMPF2	AE10126	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100743	TGAGTGTCAAGCTTGGCTTCTG	AE100745	494
	XPMPF2	AE10127	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100744	TGAGTGTCAAGCTTGGCTTCTG	AE100746	495
	XPMPF2	AE10128	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100745	TGAGTGTCAAGCTTGGCTTCTG	AE100747	496
	XPMPF2	AE10129	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100746	TGAGTGTCAAGCTTGGCTTCTG	AE100748	497
	XPMPF2	AE10130	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100747	TGAGTGTCAAGCTTGGCTTCTG	AE100749	498
Antihypertensive P (membrane-bound)	XPMPF2	AE10131	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100748	TGAGTGTCAAGCTTGGCTTCTG	AE100750	499
	XPMPF2	AE10132	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100749	TGAGTGTCAAGCTTGGCTTCTG	AE100751	500
	XPMPF2	AE10133	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100750	TGAGTGTCAAGCTTGGCTTCTG	AE100752	501
	XPMPF2	AE10134	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100751	TGAGTGTCAAGCTTGGCTTCTG	AE100753	502
	XPMPF2	AE10135	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100752	TGAGTGTCAAGCTTGGCTTCTG	AE100754	503
	XPMPF2	AE10136	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100753	TGAGTGTCAAGCTTGGCTTCTG	AE100755	504
	XPMPF2	AE10137	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100754	TGAGTGTCAAGCTTGGCTTCTG	AE100756	505
	XPMPF2	AE10138	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100755	TGAGTGTCAAGCTTGGCTTCTG	AE100757	506
	XPMPF2	AE10139	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100756	TGAGTGTCAAGCTTGGCTTCTG	AE100758	507
	XPMPF2	AE10140	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100757	TGAGTGTCAAGCTTGGCTTCTG	AE100759	508
Antihypertensive P (membrane-bound)	XPMPF2	AE10141	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100758	TGAGTGTCAAGCTTGGCTTCTG	AE100760	509
	XPMPF2	AE10142	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100759	TGAGTGTCAAGCTTGGCTTCTG	AE100761	510
	XPMPF2	AE10143	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100760	TGAGTGTCAAGCTTGGCTTCTG	AE100762	511
	XPMPF2	AE10144	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100761	TGAGTGTCAAGCTTGGCTTCTG	AE100763	512
	XPMPF2	AE10145	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100762	TGAGTGTCAAGCTTGGCTTCTG	AE100764	513
	XPMPF2	AE10146	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100763	TGAGTGTCAAGCTTGGCTTCTG	AE100765	514
	XPMPF2	AE10147	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100764	TGAGTGTCAAGCTTGGCTTCTG	AE100766	515
	XPMPF2	AE10148	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100765	TGAGTGTCAAGCTTGGCTTCTG	AE100767	516
	XPMPF2	AE10149	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100766	TGAGTGTCAAGCTTGGCTTCTG	AE100768	517
	XPMPF2	AE10150	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100767	TGAGTGTCAAGCTTGGCTTCTG	AE100769	518
Antihypertensive P (membrane-bound)	XPMPF2	AE10151	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100768	TGAGTGTCAAGCTTGGCTTCTG	AE100770	519
	XPMPF2	AE10152	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100769	TGAGTGTCAAGCTTGGCTTCTG	AE100771	520
	XPMPF2	AE10153	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100770	TGAGTGTCAAGCTTGGCTTCTG	AE100772	521
	XPMPF2	AE10154	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100771	TGAGTGTCAAGCTTGGCTTCTG	AE100773	522
	XPMPF2	AE10155	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100772	TGAGTGTCAAGCTTGGCTTCTG	AE100774	523
	XPMPF2	AE10156	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100773	TGAGTGTCAAGCTTGGCTTCTG	AE100775	524
	XPMPF2	AE10157	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100774	TGAGTGTCAAGCTTGGCTTCTG	AE100776	525
	XPMPF2	AE10158	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100775	TGAGTGTCAAGCTTGGCTTCTG	AE100777	526
	XPMPF2	AE10159	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100776	TGAGTGTCAAGCTTGGCTTCTG	AE100778	527
	XPMPF2	AE10160	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100777	TGAGTGTCAAGCTTGGCTTCTG	AE100779	528
Antihypertensive P (membrane-bound)	XPMPF2	AE10161	Intn17	0	XPMPF2_X17a	CAAGTGTGGCAGCTTCTGGTGA	AE100778	TGAGTGTCAAG		

Table IX (2 of 2)

GENE DESCRIPTION	HGNC ID	SNP ID	EXON	RETCOMP	Target Name	Forward sequencing primer	forward seq name	Forward sequencing primer (BED ID NO)	Reverse sequencing primer	Reverse seq name	Reverse sequencing primer (BED ID NO)
Brahylin Receptor B2	BDRB2	AE104628	Exon3	1	BDRB2_X3-2a	TTGCTGAGACAGGAACAGTCC	AE104655	TTGCTGAGACAGGAACAGTCC	TATTCGACACCATCTGTCCG	AE104656	817
Brahylin Receptor B2	BDRB2	AE104629	Exon3	1	BDRB2_X3-2b	TTGCTGAGACAGGAACAGTCC	AE104655	TTGCTGAGACAGGAACAGTCC	TATTCGACACCATCTGTCCG	AE104656	818
Angiotensin Converting Enzyme 2	ACE2	AE10911	Intron14	1	ACE2_X14a	TTTGTGAGACAGGACAGTCC	AE109627	TTTGTGAGACAGGACAGTCC	AGTGGGATCTGTGGAGGAA	AE109628	819
Angiotensin Converting Enzyme 2	ACE2	AE10942	Intron13	1	ACE2_X13a	CAGCTGTGTGACAGAGTCCGCA	AE109631	CAGCTGTGTGACAGAGTCCGCA	AGATCTGAACGCGCTCAAGAA	AE109632	820
Angiotensin Converting Enzyme 2	ACE2	AE10943	Intron13	1	ACE2_X13a	CAGCTGTGTGACAGAGTCCGCA	AE109631	CAGCTGTGTGACAGAGTCCGCA	AGATCTGAACGCGCTCAAGAA	AE109632	821
Angiotensin Converting Enzyme 2	ACE2	AE10944	Intron13	1	ACE2_X13a	TCATTCATGTCTTCCGCGCTTCA	AE109671	TCATTCATGTCTTCCGCGCTTCA	TCCTCAGCAAAATTCGATTTGT	AE109672	822
Angiotensin Converting Enzyme 2	ACE2	AE10945	Intron12	1	ACE2_X12a	TCATTCATGTCTTCCGCGCTTCA	AE109671	TCATTCATGTCTTCCGCGCTTCA	TCCTCAGCAAAATTCGATTTGT	AE109672	823
Angiotensin Converting Enzyme 2	ACE2	AE10946	Intron12	1	ACE2_X12a	GCACACAGGAGAACACACATCA	AE109619	GCACACAGGAGAACACACATCA	CTCCGCGCAATGTCTGTATG	AE109620	824
Angiotensin Converting Enzyme 2	ACE2	AE10947	Intron16	1	ACE2_X16a	GCACACAGGAGAACACACATCA	AE109619	GCACACAGGAGAACACACATCA	CTCCGCGCAATGTCTGTATG	AE109620	825
Angiotensin Converting Enzyme 2	ACE2	AE10948	Intron16	1	ACE2_X16a	GCACACAGGAGAACACACATCA	AE109619	GCACACAGGAGAACACACATCA	CTCCGCGCAATGTCTGTATG	AE109620	826
Angiotensin Converting Enzyme 2	ACE2	AE10949	Intron16	1	ACE2_X16a	GCACACAGGAGAACACACATCA	AE109619	GCACACAGGAGAACACACATCA	CTCCGCGCAATGTCTGTATG	AE109620	827
Protease Inhibitor 4	P4	AE11101	Intron1	0	P4_X2a	GATCTGGAGGAGCTGTTCTTGG	AE109223	GATCTGGAGGAGCTGTTCTTGG	CACACTGATTAACCTGTCCGAG	AE110024	828
Protease Inhibitor 4	P4	AE11102	Intron2	0	P4_X2a	GATCTGGAGGAGCTGTTCTTGG	AE109223	GATCTGGAGGAGCTGTTCTTGG	CACACTGATTAACCTGTCCGAG	AE110024	829
Protease Inhibitor 4	P4	AE11103	Intron2	0	P4_X2a	GATCTGGAGGAGCTGTTCTTGG	AE109223	GATCTGGAGGAGCTGTTCTTGG	CACACTGATTAACCTGTCCGAG	AE110024	830
Protease Inhibitor 4	P4	AE11104	Intron2	0	P4_X2a	GATCTGGAGGAGCTGTTCTTGG	AE109223	GATCTGGAGGAGCTGTTCTTGG	CACACTGATTAACCTGTCCGAG	AE110024	831
Protease Inhibitor 4	P4	AE11105	Intron2	0	P4_X2a	GATCTGGAGGAGCTGTTCTTGG	AE109223	GATCTGGAGGAGCTGTTCTTGG	CACACTGATTAACCTGTCCGAG	AE110024	832
Protease Inhibitor 4	P4	AE11106	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	833
Protease Inhibitor 4	P4	AE11107	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	834
Protease Inhibitor 4	P4	AE11108	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	835
Protease Inhibitor 4	P4	AE11109	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	836
Protease Inhibitor 4	P4	AE11110	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	837
Protease Inhibitor 4	P4	AE11111	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	838
Protease Inhibitor 4	P4	AE11112	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	839
Protease Inhibitor 4	P4	AE11113	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	840
Protease Inhibitor 4	P4	AE11114	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	841
Protease Inhibitor 4	P4	AE11115	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	842
Protease Inhibitor 4	P4	AE11116	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	843
Protease Inhibitor 4	P4	AE11117	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	844
Protease Inhibitor 4	P4	AE11118	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	845
Protease Inhibitor 4	P4	AE11119	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	846
Protease Inhibitor 4	P4	AE11120	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	847
Protease Inhibitor 4	P4	AE11121	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	848
Protease Inhibitor 4	P4	AE11122	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	849
Protease Inhibitor 4	P4	AE11123	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	850
Protease Inhibitor 4	P4	AE11124	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	851
Protease Inhibitor 4	P4	AE11125	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	852
Protease Inhibitor 4	P4	AE11126	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	853
Protease Inhibitor 4	P4	AE11127	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	854
Protease Inhibitor 4	P4	AE11128	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	855
Protease Inhibitor 4	P4	AE11129	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	856
Protease Inhibitor 4	P4	AE11130	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	857
Protease Inhibitor 4	P4	AE11131	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	858
Protease Inhibitor 4	P4	AE11132	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	859
Protease Inhibitor 4	P4	AE11133	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	860
Protease Inhibitor 4	P4	AE11134	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	861
Protease Inhibitor 4	P4	AE11135	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	862
Protease Inhibitor 4	P4	AE11136	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	863
Protease Inhibitor 4	P4	AE11137	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	864
Protease Inhibitor 4	P4	AE11138	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	865
Protease Inhibitor 4	P4	AE11139	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	866
Protease Inhibitor 4	P4	AE11140	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	867
Protease Inhibitor 4	P4	AE11141	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	868
Protease Inhibitor 4	P4	AE11142	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	869
Protease Inhibitor 4	P4	AE11143	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	870
Protease Inhibitor 4	P4	AE11144	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	871
Protease Inhibitor 4	P4	AE11145	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	872
Protease Inhibitor 4	P4	AE11146	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	873
Protease Inhibitor 4	P4	AE11147	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	874
Protease Inhibitor 4	P4	AE11148	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	875
Protease Inhibitor 4	P4	AE11149	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	876
Protease Inhibitor 4	P4	AE11150	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	877
Protease Inhibitor 4	P4	AE11151	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	878
Protease Inhibitor 4	P4	AE11152	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	879
Protease Inhibitor 4	P4	AE11153	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	880
Protease Inhibitor 4	P4	AE11154	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	881
Protease Inhibitor 4	P4	AE11155	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	882
Protease Inhibitor 4	P4	AE11156	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	883
Protease Inhibitor 4	P4	AE11157	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	884
Protease Inhibitor 4	P4	AE11158	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	885
Protease Inhibitor 4	P4	AE11159	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	886
Protease Inhibitor 4	P4	AE11160	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	887
Protease Inhibitor 4	P4	AE11161	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	888
Protease Inhibitor 4	P4	AE11162	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	889
Protease Inhibitor 4	P4	AE11163	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	890
Protease Inhibitor 4	P4	AE11164	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	891
Protease Inhibitor 4	P4	AE11165	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	892
Protease Inhibitor 4	P4	AE11166	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	893
Protease Inhibitor 4	P4	AE11167	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	894
Protease Inhibitor 4	P4	AE11168	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	895
Protease Inhibitor 4	P4	AE11169	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	896
Protease Inhibitor 4	P4	AE11170	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	897
Protease Inhibitor 4	P4	AE11171	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	898
Protease Inhibitor 4	P4	AE11172	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	899
Protease Inhibitor 4	P4	AE11173	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	900
Protease Inhibitor 4	P4	AE11174	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	901
Protease Inhibitor 4	P4	AE11175	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	902
Protease Inhibitor 4	P4	AE11176	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	903
Protease Inhibitor 4	P4	AE11177	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	904
Protease Inhibitor 4	P4	AE11178	Intron2	0	P4_X12a	TTGCGGCGAGAACTGTGAGATAT	AE11007	TTGCGGCGAGAACTGTGAGATAT	CTACCTGACTGCCAAGTTGT	AE11008	905
Protease Inhib											

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:1)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:1)	ORCHID_SNPLT	ORCHID_SNPLT (SEQ ID NO:1)
AE100s1	TATCATTTGTGCTTATGACCG	1066	CAGGTCAGGAGAGGC	1154	CCTCATGATGTCGCTGCTCTCC	1242
AE100s10	AAACTTCATCATGAGGTACCAAG	1067	GAGGACATTTTGATTCAGACTCCTC	1155	GTGGTTTGCAAACTTACATGCAC	1243
AE100s11	ATAGAATGACTTCTCCAGAGGGA	1068	CAGCTTAACCTCTGACTGGG	1156	TGGAAGCCAGCCAGAGGT	1244
AE100s12	TCCAGGAGGACTGGCCTG	1069	GAAGGAGGCTTAACCTG	1157	AGCCAGGCCCCAGAGGTCTCCCA	1245
AE100s13	ATAGAATGACTTCTCCAGAGGGA	1070	GCTGAGAAGGAGAGAGATGTT	1158	AATTTGAGANGNCAGCCTAACCTG	1246
AE100s14	N/A	N/A	N/A	N/A	N/A	N/A
AE100s15	ACCTCTGTCTGCTGAG	1071	GATGAGGAGCAAGGGAG	1159	CCGGSTCTTCTTCANGCNTTTCT	1247
AE100s16	AAAGAAGAGAGAGAGAGAGAA	1072	GTGTAGGAATAGAGAGGGGTATAGG	1160	AGAAAGCTTGCTCAGGAGATCAGC	1248
AE100s17	N/A	N/A	N/A	N/A	N/A	N/A
AE100s18	AACACAGAGAGCCCTCTCA	1073	GATCCAGAGCATCTCTATGAGC	1161	TACCTTAATAATAATAAAGCCAG	1249
AE100s19	N/A	N/A	N/A	N/A	N/A	N/A
AE100s2	ATAGAATTTGAGGGCAGGG	1074	GTATCTTTTGCAGTTCACTCCCC	1162	GCAACAAGTCTCTTTNCAGAACAGTC	1250
AE100s20	TACCACAGAGGGGACTGG	1075	GATTGAGTACTGGAGCTGG	1163	AGACTTCACCTCTTGGCANCCTTGGCTT	1251
AE100s21	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGCTTAAAGCAGACAAATTT	1076	GAGTGGGCTCAGGGACT	1164	CTGCATGTTGCTGAAGGGTGAAGA	1252
AE100s24	CGCTATCTGATCTCCATCATCT	1077	CCGCACCTGGAGTTGGGG	1165	TTNGAGGCTGTGGCTNCACACAGACT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAGTAAGATTTGTTGAGGAAGG	1078	GAGCCCCAAAAGTGTATGTA	1166	TTACCTTANGGCTGACCTNCCAGGAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A	N/A	N/A
AE100s30	TATCTTTCTTCACTTGGCACCA	1079	CAATGGACAGAGAGAGGGG	1167	TCACCTGGCTCTCACCAGATTC	1255
AE100s4	TCCCTGCTGCTTCCCGG	1080	AATATTTGTGCTGATTTACCAGATAG	1168	TATTTACAGCCTGACAGGCTCAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGATGATGAGTGTAGTG	1081	CTTTGCTATTTTCATCTCTGTA	1169	ACCTTCATGAGGGTATATTAAG	1257
AE100s7	ATCCAGTAATGGCAAGCCNG	1082	GTCAGCCTTAGGCTAACAGTTTG	1170	AAGAGTTTGTGTTGAGGAAGGTTT	1258
AE100s8	GCAATCTCAGCTCTGCTG	1083	CAGGTCTGGGGGACACAGTA	1171	GTAAGGAGGCTCTONATNCCAGGGG	1259
AE100s9	AAACTAGAAAGACAGAAAGCAC	1084	TTTCAGAGACTGGCAGGAG	1172	CACAGCTAGAGAGATTCACAGAAA	1260
AE103s1	AACTTCTTTGCTTCACTAACAGCT	1085	GATGAAGATATTGGACAGACTTTTAG	1173	CCAGTAATTTATGCTCTTTTGGGCC	1261
AE103s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGATGTTTACCAATT	1086	GACTCTGAGCTCTCTGCCTC	1174	ATCCTGAATTTATCCAAAGTGGCCCT	1262
AE103s12	N/A	N/A	N/A	N/A	N/A	N/A
AE103s13	CCACCGAGTTTCTGTAATTTG	1087	CTTTGAATGACAAATGGAGTGTATAGA	1175	CAGCAGGAACAAATAACAGTATC	1263
AE103s14	TGTCATAGCAGCAGCAGAA	1088	CCTGCGAGTTAGCTAGAAAGC	1176	ACAAGTATCTGCTAATGCTCTCTTA	1264
AE103s2	TGCAATGCTCCAGAGCC	1089	CAACAGACAAAGAGTTCC	1177	CTGGAGCTCTGCTNACAGAGTCTGCC	1265
AE103s3	ACTTTCTGCGGGAATTAAACA	1090	ACCCGCCATCTACGGGA	1178	TGAACCAANANGCTTGGCTTTCTTATC	1266
AE103s4	N/A	N/A	N/A	N/A	N/A	N/A
AE103s5	N/A	N/A	N/A	N/A	N/A	N/A
AE103s6	TTCTGGGAGAGATATCTGGA	1091	CCACGAGAGATGCTGATG	1179	GAGCCCTCTCTGCGGTGATCAAA	1267
AE103s7	N/A	N/A	N/A	N/A	N/A	N/A
AE103s8	ATCTGACATCCAGCCT	1092	GTAGTTGAGAGAGAGATCGC	1180	AGATCTGAACATCAACCGCTGCATC	1268
AE103s9	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1	GAGAGCAATTAATCTGTTTTTGATAA	1093	CTCACCTGCTGCTGTTG	1181	CACTGGGCAATGNGGNGGCTCCGCC	1269
AE104s10	GTTGGGCGCTCAGGGTG	1094	GTGGCGGTGTGAGCACC	1182	GTNGAATGACAGGTGAAAGGAGCCA	1270

SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:1)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:1)	ORCHID_SNIPPIT	ORCHID_SNIPPIT (SEQ ID NO:1)
AE104s11	TTGATGTGAATGCTTCCTG	1095	GCCCTATGATGATGTAGATG	1183	TTACAACATACAGCNCATTTAGTCTT	1271
AE104s12	ATTTTCTCTTTGGATGTGAATG	1096	CGGCCCTATGATGTGTA	1184	TAACAGCTCATTTAGTCTTTCACAG	1272
AE104s13	GCCATTTGGCGCAGAGCTC	1097	AAAAAAGAGGCTGTGTTTGTCA	1185	GGCAGTCAATTCAGACACAGAGAC	1273
AE104s14	AAGTGATAGTCTCCCT	1098	AAGTGCCCATGATGAGC	1186	CCCTAGAGAGTGTGAAAGGAATG	1274
AE104s16	GATGATGAGTGGAGGAGG	1099	CAGTGATGGGAATTTCAATATCC	1187	ATTCCTTCACTCATTTATATNAACAAA	1275
AE104s17	GATGGAACAGATGAAGAGAGG	1100	CATTAATGCCCTCTCTCCAT	1188	TACGTTGAGCGATGAGCCAGGTT	1276
AE104s18	AGAAGAAAGATGTTAGATGCA	1101	CATTGAGTCAGGAGCATCTCAT	1189	ACAGGCTGGGATGTCNAATATACAC	1277
AE104s19	TAACCTAGTAACTGAGGAATCCCTTT	1102	CACTCTGAGTCAAAATGTTCTCTC	1190	GTGCTGGGCACGAGTCTCTCAC	1278
AE104s2	GAGGCAATTAATGTCTGTTTTTGATAA	1103	CTCACCTGTCTCTCTGATG	1191	GTACAGGAGGGGNCACCTGGCGCGG	1279
AE104s20	TTTACACTCCACAGGCTGAG	1104	CTCTTCCACAGATCCACTGG	1192	TTTTTGNAGCTTTAAACACCTTCCCTTC	1280
AE104s21	GGATTTCTTGTATGCCACGATAC	1105	CATACATCTCCGAGAAACGG	1193	GCAGAAGCTGTCTCTTTCTCTGGGT	1281
AE104s22	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGGAGTGGCGGCG	1106	GCAGGATGCGAGGCTCAG	1194	GAAGTCCCAGGAGGCTGNTGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A	N/A
AE104s26	TGAATAGATTAAGAAACCCAGGG	1107	GTCTCTCTCTCTCTCTCTCTCT	1195	CATTGACCAACAACTGGATGCG	1283
AE104s27	TCGACCGTCTCGTCCGAAAC	1108	GAAGAGAGAGGACCATCTCCA	1196	GCTTTCTGCTGTGTCAGTGCCTCAGTC	1284
AE104s28	N/A	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A	N/A
AE104s30	TTTGAAGGAGGGAATC	1109	CAACCTCAGCTCCAGC	1197	GAGCGAAGGCTGCTGCTGAGGTGATG	1285
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGATACATGCTAGGAGCT	1110	GTCTGGACCCCAATGTTCTAT	1198	ACCTTTTGTCTGATTTTTCACCTGTA	1286
AE104s34	ACACTGGTCTTCACACCG	1111	GTACATGTGAGGCACTCTTACGC	1199	GGCTCCCAATGATGATCTGCTCCA	1287
AE104s35	N/A	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTTCTGCTGCATATCA	1112	CATCTTGAAGAACTCAAGACTCA	1200	ACCACAGCACCTGCTGACGCTCTC	1288
AE104s4	AGTGAGGCTTGGAGTGCA	1113	CTTTGATGAAAGAGGAGCA	1201	AGGTTTCAGGGAGACTGGATGAGG	1289
AE104s5	TGCAGGTTGACAGGAGA	1114	CAAGAGAGGCTCTTTGGAT	1202	GCTGGGATGAGTCTGGGTGCTGCT	1290
AE104s6	GGCTCAACATGTGGAAATGC	1115	CAAGAGGCTCTGCCCA	1203	GTCTCTGGAGAAATAACTGTGCTG	1291
AE104s7	AACGTGGCCACAGGCT	1116	AACCCCTTACCACACG	1204	CCCTCTCTCCAGCTCTGCTCCACAA	1292
AE104s8	ATGTACGTAGCACCTTTGCTTT	1117	GGAGACCAAGGTTCCAGCTC	1205	GAAGGGGAACTGAGGCGGAGCAG	1293
AE104s9	TATTTCTAGACCTCAGTCTTTTCTTATAG	1118	GAAGTCTGTGAGGTTAAGG	1206	AAGGTCTCTAGCTATATATGAGCATC	1294
AE105s1	GAGAGACCTCTGAAGGGGG	1119	AGGTCTTCACTGCTCTGCA	1207	CCAGCGCTGGGGAAGAAAGGACA	1295
AE105s2	ATTGTGACAGAGGGTGGGG	1120	CAAACTCAGATTTGGAGAGC	1208	GAGATCGGTAGAGAGACTGTTAAG	1296
AE105s3	N/A	N/A	N/A	N/A	N/A	N/A
AE105s4	CCGAAGGAAGGTGCGCAA	1121	TTGAGTTGGTTGCGCAA	1209	AAGCTGAANCTCNAGGATGGGTTCA	1297
AE105s5	TGTTGGGGATGCTTTGG	1122	GATGCTGAATGGGAAAGG	1210	AAGCTCTACCAAGCTTCTCAG	1298
AE105s6	ATCTCTGGCCCGCACCC	1123	CATATCTGCTCCCATGAGAC	1211	GGAACTTGTCTCTGCTGCTCCAGACA	1299
AE106s1	TATCAAGGCCACAGCCG	1124	CACACAGATGATGATGAGCC	1212	TACTGGGAGAGACAGCGGATGGG	1300
AE106s2	ATGGTCTCTGTGTGATGATAGC	1125	CATCATACATCCCTCTGAGC	1213	CCAGCAGAGAGACGACGACCA	1301
AE106s3	ATGCTCTCTGTGTGATGATAGC	1126	CTACCAAGGAGGATGCTCTG	1214	CCAAGCGAAGGTGAGCAGGGG	1302
AE106s4	TGCAGATTTATCTCGAAATGA	1127	CTGCTGACTCAACCAAACTCACT	1215	AGGTGGAGCCACTTTTCTCCAA	1303
AE106s5	AAAAGCTGTCGACCTTTTATTT	1128	TCAAACTCTCAATCTTCTCTATCT	1216	TCCCTATCTTTGACNCTNATGCTGT	1304
AE106s6	TTTGAGTCACAGCATGAGG	1129	CATGGAATTCCTCTCATCTG	1217	ACCACTACTGACCTTTTNGCAGTGC	1305
AE106s7	ATGGTCTTGGATCCTTCCTG	1130	CCACGAGAGGAGCCAG	1218	AGAGCATGTGAGGTGAGTTCAGGGA	1306

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNIPIT	ORCHID_SNIPIT (SEQ ID NO:)
AE106s8	N/A	N/A	N/A	N/A	N/A	N/A
AE106s9	N/A	N/A	N/A	N/A	N/A	N/A
AE107s1	GTTCGAGTCTCATTTCCAGATGATC	1131	ACACACAGCATGAAGTGTGTGCAC	1219	CAAAATCTGCCTTAATGATGAGTGC	1307
AE107s2	AGCATCGACAGAGAAATTGTATG	1132	CTTCCCTGGCCCTTTCTC	1220	TCCTCTTGACRCAGGAGTCCCATCCC	1308
AE107s3	CCCTGATGATCATCATCAGATG	1133	CATACAAATTCCTGTGTTCGATGC	1221	GCTGTGAAGTTCGCGGAGTTGCCAC	1309
AE107s4	ATCGACACAGAGAAATTGTATGCG	1134	GGGAGAAAAGGGCTGCA	1222	AAGCGGGGATGGGACTCTCTG	1310
AE107s5	ACCTGGACCCACTCGCT	1135	CTTTTCCCCACCTGCTG	1223	TGNGGCCACCCAGCTGTGTCA	1311
AE107s6	CCAGTAATCAAAATGTGCATCC	1136	CAGCTCAGCCGAGTGGG	1224	ATGTGTGCACGTTCTGCTCATCACC	1312
AE109s1	AATAGCTTATCAATTAAGGAATAGGTTACTTT	1137	GAATTGATTTATTTTGTAGTGCACATGC	1225	ATCTGGAACTTATAGTNTTGAAGAA	1313
AE109s2	GGGGGTTCAAGGCCCTTTT	1138	GCAAAATTTAGCCAGTCAAGNCA	1226	GAGGGTTCCAGANGTACNTATATTTA	1314
AE109s3	TGGGGCCAAAGGAGTAG	1139	GCTGAAGACCCAGACAGATTC	1227	AGCTAGCAGGAATGGGTGTGAA	1315
AE109s4	GTGTGAAACACACATATCTCAAT	1140	TGGAAAAGTTTGTAAACCCAGATATC	1228	TCATAATCAGCNANTNAAANTTAGTAGC	1316
AE109s5	GTGTTCACCTGCAAAATTAAGATATTAACA	1141	ACATGGCAAAGAGTAATTTGCTG	1229	GAATTTTGTCTGAAGAGATCTGTA	1317
AE109s6	AACTCAAATCAAGATTATTCCTCCCTG	1142	GTACCAAAATACACAACTAAACAGTATT	1230	CACATGTAAATGACTCAGAAATAG	1318
AE109s7	CCCTCACCTTAGATGAAGTAAAA	1143	TTTGAACCCAGAAATCTCTTTAAATTT	1231	TTCAAGTTCTAGGAATNATATCAGACAC	1319
AE109s8	N/A	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCTCACTCAAAAAGGCAATT	1144	TGCTCTCCCTGCTCATTTG	1232	CTTGTAAANAAGCCCAATNAATTTCTTC	1320
AE110s1	N/A	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTTGGACGTGGATGAG	1145	ATGTGGCGATTTGGTCTGG	1233	GGNTGGCACCGAGNTGCGAGCAGCCAC	1321
AE110s11	CACCTCTGTCACACTCTCA	1146	CATGTTGTCATTCAGGAATTTTG	1234	AACTCNCOCGNCATGGCTGGAAACA	1322
AE110s12	AGATTTGGGGGAGAACTGG	1147	CAGTAGACTGGTCTTTGTATTTTACC	1235	TTTCTTGGACAGATGTTNATTTATGAA	1323
AE110s2	CTGTACCTTCTTTTCATCTTCCCTT	1148	GCAAGTCAATGGGCACCC	1236	CCGAGCTGTTGTCTCTCATCAACATA	1324
AE110s3	AAGGNGGCTCTGCCAG	1149	GATGCACTCTAGCTTCTGTGTAATAAT	1237	GATCTGCTTGTCTTCAATANTCTAATG	1325
AE110s4	N/A	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCAGACACCGTCAAGAA	1150	GATTTAGCATATACCAATGATCTGACTCT	1238	GAGGAAGATTTGTGATTTGCTCAG	1326
AE110s6	GTCAAACTTAATGCTGAAGTGG	1151	TTTCAGATGAGTTGATTTTCATTAGTGC	1239	AGACCCCTAAATAAATACTCTGAGGAT	1327
AE110s7	AGGTCAAACTAAATAGGCTGAAA	1152	CACCTGTCTTTTCAGATGAGTGTGATTTTC	1240	TAAACCATATAAAGCAGCTCCACAGA	1328
AE110s8	AGAACTGGAGTATCTTTCTTGG	1153	CTGTAGAGTCTCAGTAGACTGCTCTTGG	1241	TATGAAGCGGTACCACTTCTATCCCC	1329
AE110s9	N/A	N/A	N/A	N/A	N/A	N/A

SNP_ID	GBS_LEFT	GBS_LEFT (SEQ ID No.1)	GBS_RIGHT	GBS_RIGHT (SEQ ID No.1)
AE100s1	TGTTAAACGACGCGCCAGTGTCTTCCTCTCCCTCACT	1330	CAGGAAACAGCTATGACCCAGAAAGCTGTGGGTCTC	1451
AE100s10	TGTTAAACGACGCGCCAGTGAGGATCAGCTGATTTGACGT	1331	CAGGAAACAGCTATGACCCAGCCAGCCAGCAAAATC	1452
AE100s11	TGTTAAACGACGCGCCAGTGTTCCTGGGCTTTACCTCTCTC	1332	CAGGAAACAGCTATGACCTAGGCTCTGACGAGAGCA	1453
AE100s12	TGTTAAACGACGCGCCAGTGTTCCTGGGCTTTACCTCTCTC	1333	CAGGAAACAGCTATGACCTAGGCTGTGAGCAGAGACA	1454
AE100s13	TGTTAAACGACGCGCCAGTGTCCAGGTCAGAGATTAACAGAC	1334	CAGGAAACAGCTATGACCTAGGCTCTGACGAGAGACA	1455
AE100s14	TGTTAAACGACGCGCCAGTGTAGGACATTCGACACCTCGG	1335	CAGGAAACAGCTATGACCTAGCCATGACATACCACAGAG	1456
AE100s15	TGTTAAACGACGCGCCAGTGTCTTCAACCCCTCATACAG	1336	CAGGAAACAGCTATGACCTAGCCATGACATACCACAGAG	1457
AE100s16	TGTTAAACGACGCGCCAGTGTGATGATCTTTGCCACTGCG	1337	CAGGAAACAGCTATGACCCAGCCAGCTTAGGAAAGGCC	1458
AE100s17	TGTTAAACGACGCGCCAGTGTGACGACAGACAAATGATGTAG	1338	CAGGAAACAGCTATGACCTTGCTCTCTCTGAAATCTC	1459
AE100s18	TGTTAAACGACGCGCCAGTGTATCCAGGAGATGAGTGGAATG	1339	CAGGAAACAGCTATGACCAATACGAGATGTTGTTGGA	1460
AE100s19	TGTTAAACGACGCGCCAGTGTGAGGAGATGACGTGTGATG	1340	CAGGAAACAGCTATGACCTTGCTTCTTCTGAAACCC	1461
AE100s2	TGTTAAACGACGCGCCAGTGTGTAAGCCCTTTGACAGAGT	1341	CAGGAAACAGCTATGACCTTGTCTGAGCTACAGGCC	1462
AE100s20	TGTTAAACGACGCGCCAGTGTCTGTAAGAACGCCACAGAAAT	1342	CAGGAAACAGCTATGACCTGTGTGAAGCCAGCTCGA	1463
AE100s21	TGTTAAACGACGCGCCAGTGTGAGGCTCCAGACTCTCTGTGT	1343	CAGGAAACAGCTATGACCCGAGCGAGCTGTGTGAGAGT	1464
AE100s22	TGTTAAACGACGCGCCAGTGTGCTGTAGAACCTTTGCTGA	1344	CAGGAAACAGCTATGACCTGTCTCTTTGGGGTTT	1465
AE100s23	TGTTAAACGACGCGCCAGTGTGACCAAGCTATCAATGCTGTT	1345	CAGGAAACAGCTATGACCAAAACCCAGAGGCAAGTT	1466
AE100s24	TGTTAAACGACGCGCCAGTGTGCTGCTCAACACAGAACTCT	1346	CAGGAAACAGCTATGACCCGCACTTTGCTCCAGATCT	1467
AE100s25	TGTTAAACGACGCGCCAGTGTGAGAACAGTGTCTCTCCCG	1347	CAGGAAACAGCTATGACCCCATGCTGAACTGTGTGAG	1468
AE100s26	TGTTAAACGACGCGCCAGTGTGCTGTGCTTGGCTTTACTTTC	1348	CAGGAAACAGCTATGACCCGCACTCTCCCTACTCCGA	1469
AE100s27	TGTTAAACGACGCGCCAGTGTGAAACACAGAGGGGTTTAG	1349	CAGGAAACAGCTATGACCGTCTGCAATATCCACACT	1470
AE100s28	TGTTAAACGACGCGCCAGTGTGTATACCAACACCTCTGG	1350	CAGGAAACAGCTATGACCAACAGCCAAATTTCTATG	1471
AE100s29	TGTTAAACGACGCGCCAGTGTGAGATGAGAAAGCAGCTAG	1351	CAGGAAACAGCTATGACCGTTCCTCAACCTCTGTT	1472
AE100s3	TGTTAAACGACGCGCCAGTGTGTGTAAGAAAGCAGACAGA	1352	CAGGAAACAGCTATGACCTGTCTGCTGGCCTGAAAT	1473
AE100s30	TGTTAAACGACGCGCCAGTGTAGAAATTTGAGGCCATCACT	1353	CAGGAAACAGCTATGACCTCTCTTCTTCAACAGAT	1474
AE100s4	TGTTAAACGACGCGCCAGTGTAGCTGTAAAGATCCCTTCAT	1354	CAGGAAACAGCTATGACCGTTCCTGAAACACTCTT	1475
AE100s5	TGTTAAACGACGCGCCAGTGTGAAAGGCTCCCTCTCTCTC	1355	CAGGAAACAGCTATGACCTTGCNAATGCGGTAGTCT	1476
AE100s6	TGTTAAACGACGCGCCAGTGTCAAGGTGGCCAGCTCTCGGTA	1356	CAGGAAACAGCTATGACCTGTCCGAGATTTCTCTAC	1477
AE100s7	TGTTAAACGACGCGCCAGTGTCTATAGCACCCCTATTTGA	1357	CAGGAAACAGCTATGACCTGCGAGCGCATATTTTC	1478
AE100s8	TGTTAAACGACGCGCCAGTATCCGAAGACAGGGATTTCAAT	1358	CAGGAAACAGCTATGACCTGTCTTCTACTGCTCTT	1479
AE100s9	TGTTAAACGACGCGCCAGTATCCGAAGACAGGGATTTCAAT	1359	CAGGAAACAGCTATGACCTGTGGGAGTAGTGTCTG	1480
AE103s1	TGTTAAACGACGCGCCAGTGTCTTGTCTCTCTGGAATTTCT	1360	CAGGAAACAGCTATGACCTCAATGCTGTGTTTTAATTT	1481
AE103s10	TGTTAAACGACGCGCCAGTGTCCCCAGATCTGCAACATCAC	1361	CAGGAAACAGCTATGACCCGACCTGCTTGTACCTGGA	1482
AE103s11	TGTTAAACGACGCGCCAGTGTGAACACAGAGCTTGGCTTTC	1362	CAGGAAACAGCTATGACCTCAATGCTGTGTTCCCTG	1483
AE103s12	TGTTAAACGACGCGCCAGTGTACTTCCAGACTCAAGGGAT	1363	CAGGAAACAGCTATGACCTCTCTGTATTTCTCTGGCA	1484
AE103s13	TGTTAAACGACGCGCCAGTGTGATGATCTTCCACTTTGGT	1364	CAGGAAACAGCTATGACCTGTGTGTGTTTCAATGCAAT	1485
AE103s14	TGTTAAACGACGCGCCAGTGTCTTGTGCTTCCCTCCCTGA	1365	CAGGAAACAGCTATGACCTGTGTGTGTTTCTCTGGCCT	1486
AE103s2	TGTTAAACGACGCGCCAGTGTCTGATCTGTGCACTCTCTTG	1366	CAGGAAACAGCTATGACCTGTGTGTGTTTCTGTGCCCAAT	1487
AE103s3	TGTTAAACGACGCGCCAGTGTAGGACCAAGGTTCTGGAACT	1367	CAGGAAACAGCTATGACCTGTGATTTCTCTGGCCT	1488
AE103s4	TGTTAAACGACGCGCCAGTGTCCGGAACACAGACAATTA	1368	CAGGAAACAGCTATGACCAAGCAGCATGGATCAG	1489
AE103s5	TGTTAAACGACGCGCCAGTGTCTTCCAGACTCAAGGGAT	1369	CAGGAAACAGCTATGACCTCTCTGTATTTCTCTGGCA	1490
AE103s6	TGTTAAACGACGCGCCAGTGTCTTGTGGGACAGAGATATC	1370	CAGGAAACAGCTATGACCTGTGTGTGTGAGGAGAAACC	1491
AE103s7	TGTTAAACGACGCGCCAGTGTCTTGTGGGACAGAGATATC	1371	CAGGAAACAGCTATGACCTGTGTGTGAGGAGAAACC	1492
AE103s8	TGTTAAACGACGCGCCAGTGTCTTGTGGGACAGAGATATC	1372	CAGGAAACAGCTATGACCTGTGTGTGTTGCTATGCC	1493
AE103s9	TGTTAAACGACGCGCCAGTGTCTTGTGGGACAGAGATATC	1373	CAGGAAACAGCTATGACAGATTTCTCCAGAAAGGCA	1494
AE104s1	TGTTAAACGACGCGCCAGTGTCTTGTAAAGAGAGGCTCAG	1374	CAGGAAACAGCTATGACCGACTTTTGACCAACACCG	1495
AE104s10	TGTTAAACGACGCGCCAGTGTCTCAGCACTGTGATCCTTC	1375	CAGGAAACAGCTATGACCGGTCTGATGATCTGAT	1496

AE104s11	TGTAAACGACGGCCAGTTCGGAGTGTGTACAAATGCT	1376	CAGAAACAGCTATGACCGAGGCTGTGTTTGTCA	1497
AE104s12	TGTAAACGACGGCCAGTGTGTATGCAAAACCTCATCCA	1377	CAGAAACAGCTATGACCGAGGCTGTGTTTGTCA	1498
AE104s13	TGTAAACGACGGCCAGTGTGTATACCAATGATAGGC	1378	CAGAAACAGCTATGACCTGGAGGAAAGAAACAGG	1499
AE104s14	TGTAAACGACGGCCAGTGTGTATAGCTCTCCAGTCTAGCCC	1379	CAGAAACAGCTATGACCAATTCCTTAATCGGTCTTG	1500
AE104s15	TGTAAACGACGGCCAGTGTGTATAAAGAGGTCTGACCCAC	1380	CAGAAACAGCTATGACCTAGACCTAGATCATAGGGCCA	1501
AE104s16	TGTAAACGACGGCCAGTGTGTATACCAATGCAATTTAT	1381	CAGAAACAGCTATGACCGCCACTTGTTCATCTACT	1502
AE104s17	TGTAAACGACGGCCAGTGTGTATGAGGAATCCCTTTGACTCAC	1382	CAGAAACAGCTATGACCGATGAGCAATGTCTGG	1503
AE104s18	TGTAAACGACGGCCAGTGTGTATCTTCAACTGTGTGCC	1383	CAGAAACAGCTATGACCGATGAGCAATGTCTGG	1504
AE104s19	TGTAAACGACGGCCAGTGTGTATTAAGAGGGCGCTG	1384	CAGAAACAGCTATGACCGATGAGCAATGTCTGG	1505
AE104s20	TGTAAACGACGGCCAGTGTGTATGAGGGAGTCTTCT	1385	CAGAAACAGCTATGACCGCCACCCATATAACTGAT	1506
AE104s21	TGTAAACGACGGCCAGTGTGTATGTAACAGTGGGC	1386	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1507
AE104s22	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1387	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1508
AE104s23	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1388	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1509
AE104s24	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1389	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1510
AE104s25	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1390	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1511
AE104s26	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1391	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1512
AE104s27	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1392	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1513
AE104s28	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1393	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1514
AE104s29	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1394	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1515
AE104s30	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1395	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1516
AE104s31	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1396	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1517
AE104s32	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1397	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1518
AE104s33	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1398	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1519
AE104s34	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1399	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1520
AE104s35	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1400	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1521
AE104s36	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1401	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1522
AE104s37	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1402	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1523
AE104s38	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1403	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1524
AE104s39	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1404	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1525
AE104s40	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1405	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1526
AE104s41	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1406	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1527
AE104s42	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1407	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1528
AE104s43	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1408	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1529
AE104s44	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1409	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1530
AE104s45	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1410	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1531
AE104s46	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1411	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1532
AE104s47	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1412	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1533
AE104s48	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1413	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1534
AE104s49	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1414	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1535
AE104s50	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1415	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1536
AE104s51	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1416	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1537
AE104s52	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1417	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1538
AE104s53	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1418	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1539
AE104s54	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1419	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1540
AE104s55	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1420	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1541
AE104s56	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1421	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1542
AE104s57	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1422	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1543
AE104s58	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1423	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1544
AE104s59	TGTAAACGACGGCCAGTGTGTATGAGCCCAATGATATAAT	1424	CAGAAACAGCTATGACCTTGCAGCAAACTGAGAA	1545

AE107s2	TGTAATAACGACGGCCAGTCTCTGACAGAGCTCTGCTATAC	1425	CAGGAACACGCTATGACCATTTTGAGGTCCACACA	1546
AE107s3	TGTAATAACGACGGCCAGTCCAGTCTTCATGTCAGT	1426	CAGGAACACGCTATGACCGGAATATGAGACTACGAA	1547
AE107s4	TGTAATAACGACGGCCAGTCTCTGACAGAGCTCTGATAC	1427	CAGGAACACGCTATGACCAAGTCTGTACCTCTCTG	1548
AE107s5	TGTAATAACGACGGCCAGTCTCTACCCCTAGTAATAATCAA	1428	CAGGAACACGCTATGACCACTCTCAGCCTCAGAC	1549
AE107s6	TGTAATAACGACGGCCAGTCTGCGTCTGAGTCTGCTTAT	1429	CAGGAACACGCTATGACCTCTGTTGCTCTGCACTCTG	1550
AE109s1	TGTAATAACGACGGCCAGTCTGACGAGTCAATTGAAGGA	1430	CAGGAACACGCTATGACCATGACAGCAACCAAGCATC	1551
AE109s2	TGTAATAACGACGGCCAGTCTCAAGTCTGAGCAGTGGCC	1431	CAGGAACACGCTATGACCGACCATACACAAATTGG	1552
AE109s3	TGTAATAACGACGGCCAGTCTAATGCTGTCAACATAG	1432	CAGGAACACGCTATGACCAATGATGTAAGGCA	1553
AE109s4	TGTAATAACGACGGCCAGTCTGACAGAAATATAACACTGA	1433	CAGGAACACGCTATGACCTCTTCAGCAAAATTTCC	1554
AE109s5	TGTAATAACGACGGCCAGTCTTCTGTGATATCTGGG	1434	CAGGAACACGCTATGACCTCGACAGTGGGAAACT	1555
AE109s6	TGTAATAACGACGGCCAGTCTGCGCATGTGTAACCTGCG	1435	CAGGAACACGCTATGACCTCCCTCCCATGCTCTCT	1556
AE109s7	TGTAATAACGACGGCCAGTCTGTCATGTCATCTGTGTT	1436	CAGGAACACGCTATGACCTCCCTCCCATGCTCTCT	1557
AE109s8	TGTAATAACGACGGCCAGTCTGTCATGTCATCTGTGTT	1437	CAGGAACACGCTATGACCACTGTAATGTATAGGCA	1558
AE109s9	TGTAATAACGACGGCCAGTCTTCTCAAAATGCGATTTCT	1438	CAGGAACACGCTATGACCTTTCTTCTTGGCTTTT	1559
AE110s1	TGTAATAACGACGGCCAGTCTGAGCATGTCTAGTTTGAAT	1439	CAGGAACACGCTATGACCTCTGCTTGGTGGACAGA	1560
AE110s10	TGTAATAACGACGGCCAGTCTGCTGTGTTATCTCCCG	1440	CAGGAACACGCTATGACCTCTGCTTGGTGGACAGA	1561
AE110s11	TGTAATAACGACGGCCAGTCTGCTGTGTTATCTCCCG	1441	CAGGAACACGCTATGACCAATCCACAATCTTCCCTC	1562
AE110s12	TGTAATAACGACGGCCAGTCTGAGTCTATGGAAGTGAATTA	1442	CAGGAACACGCTATGACCACTTTAGTTTGAAC	1563
AE110s2	TGTAATAACGACGGCCAGTCTGAGTCTGAGTCTGTTCTG	1443	CAGGAACACGCTATGACCTTTGCTTGGTGGGGA	1564
AE110s3	TGTAATAACGACGGCCAGTCTTCTCAATCATCTTCTGGG	1444	CAGGAACACGCTATGACCTGACGACTTACTTTGGA	1565
AE110s4	TGTAATAACGACGGCCAGTCTCAGAGCAACCTCTGAAG	1445	CAGGAACACGCTATGACCGGAGCCAGAAATGAGGA	1566
AE110s5	TGTAATAACGACGGCCAGTCTTTCGAAAATTCCTGAATGA	1446	CAGGAACACGCTATGACCAAGGTGCTCAACCTTA	1567
AE110s6	TGTAATAACGACGGCCAGTCTTCTGTCTACGGGGTAACA	1447	CAGGAACACGCTATGACCTCCCAACAGCAGCAAT	1568
AE110s7	TGTAATAACGACGGCCAGTCTTCTGTCTACGGGGTAACA	1448	CAGGAACACGCTATGACCTCCCAACAGCAGCAAT	1569
AE110s8	TGTAATAACGACGGCCAGTCTTCTGTCTACGGGGTAACA	1449	CAGGAACACGCTATGACCTCCCAACAGCAGCAAT	1570
AE110s9	TGTAATAACGACGGCCAGTCTTCTGTCTACGGGGTAACA	1450	CAGGAACACGCTATGACCTTAAGTGAACCTGCCCCAAA	1571

Table XIII
Candidate Angioedema Susceptibility Genes

Chromosome	Gene	Gene ID
14	Bradykinin B2 Receptor	BDKRB2
19	Tissue Kallikrein	KLK1
X	Aminopeptidase P (Membrane Bound)	XPNPEP2

Table XIV
Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events

Gene ID	SNP ID	Sample or Subgroup	Scores Test	DF	Probability	Estimate Type	A,a ¹	Copies of Rare Allele	Odds Ratio (OR) ²		OR		Upper 95% CL		p(a) ³
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300	Asymptotic	A,T	1	3.41		1.3238		8.7969		0.28
					0.0251	Exact			3.37		1.2261		10.2718		
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64		1.4211		22.3807		0.09
					0.0062	Exact			5.64		1.2422		34.7611		
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95		1.9838		+INF		0.28
		Angioedema-like	11.39	2	0.0022	Exact		2	10.82		1.3105		+INF		0.22
		Overall	10.72	2	0.0047	Asymptotic		2	11.11		1.2687		97.2709		0.23

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.